



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 151069

TO: Terra Gibbs
Location: rem/2c8/2c18
Art Unit: 1635
Tuesday, April 19, 2005

Case Serial Number: 10/029115

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

Bob
barbara.obryen@uspto.gov

Search Notes

Terra,

I tried a bunch of different changes to our standard parameters, but was not able to get the % match as high as you needed it to be.

Barb

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: TERRA COTTA GIBBS Examiner #: 79523 Date: 4/15/05
Art Unit: 1635 Phone Number 30 2-2058 Serial Number: 10/029/115
Mail Box and Bldg/Room Location: Rensen Results Format Preferred (circle): PAPER DISK E-MAIL
2C8

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Seq 1 & 2 vs AB035698
attempt to get % match above 98%

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher

ASB

.....

.....

7

.....

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g8n4c8 (1-1332) x ab035698 (1-3888)

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 QY 21 ProAlaGlyIlePheGluLeuValGluValAlaGlyAsnGlyThrTyrglyGlnValTyrg 40
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 ; VERSION AB035698.1 GI:6970477
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 ; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ; REFERENCE
 ; 1 (bases)
 ; Dan.I., Watanabe.N.M., Kobayashi.T., Yamashita-Suzuki.K.,
 ; Fukagaya.Y., Kajikawa.B., Kimura.W.K., Nakashima.T.M.,
 ; Matsumoto.K., Nimomiya-Tsuji.J. and Kusum.A.
 ; Molecular cloning of MINK, a novel member of mammalian GCK family
 ; kinases, which is up-regulated during postnatal mouse cerebral
 ; development


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Db 1308 CAGAGCTGCAATGCTCCAGCGCGCTGCTCTCTCTGCTGAGCTTCCGCTGCTC 1249
Qy 924 -----LysGlyGlnSerProProSerLysAsp----- 932
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Search completed: April 15, 2005, 16:51:31
 Job time : 31 secs

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US-10-029-115-2 (1-1312) x ab035698 (1-3888)

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 ; REFERENCES
 ; 1 (sites)
 ; AUTHORS Dan, I., Matsuda, N.M., Kobayashi, T., Yamashita-Suzuki, K.,
 ; Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M.,
 ; Matsumoto, K., Nishimura-Tsuji, U., and Kusumi, A.
 ; TITLE Molecular cloning of MINK, a novel member of mammalian GCK family
 ; kinases, which is up-regulated during postnatal mouse cerebral
 ; development

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JOURNAL      FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE      20175403
PUBMED       10708748
REFERENCE    2 (bases 1 to 3888)
AUTHORS      Dan, I., Matanabe, N.M. and Kusumi, A.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
              Organizer Project; 5-11-33 Chiyoda, Naka-Ku, Nagoya, Aichi
              460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp,
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VERSION AB035698.1 GI:6970477
KEYWORDS
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ORGANISM Homo sapiens
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REFERENCE 1 (bases)
AUTHORS Dan.I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K., Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M., Matsumoto,K., Niimoriya-Tsuiji,J. and Kusum,A.
TITLE Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development

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JOURNAL      FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE      20175403
PUBMED       10708748
REFERENCE    2 (bases 1 to 3888)
AUTHORS      Dan, I., Matanabe, N.M., and Kuehni, A.
TITLE        Direct Submision
JOURNAL      Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
              Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
              460-0012, Japan (E-mail: dangbio.nagoya-u.ac.jp,
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      BEGSPSILNMPGSESTLRBELRLQENKNSKALKQOOLQOQOORDPRAHILKHLH
      QORRIEOKKEERRRVEEQRREREROKLOKEQORLEDMQALRRERERQAREBE
      YKQKQLEORSERLQROLOQEHAYLSLQOQOQOQOQOQOQOQOQLLPGDKPLHYTG
      RGNMADKPMAREBERETRMNKOQNSPLASKSGSTGPEPITQASPGPGPLSQTP
      PMQRPVPEQEGPKSLVAHRYPLKPYAAPVPSLOLDOPTRNLAAPASHDPPALP
      APRTFPGARGVIRKQNSDPTSEGPSPSPNPAWYRNEAPKVPQRTSSATLNTS
      GAGGSRPAQAVRANSDLRSDPGRMWSQVLPASHGLPDAGSLERNSQVSKKPS
      SPVLSPEKAKAPDHRSPGRPADPVLKERTLDABRPPEKKAMDYSSSEBVESSD
      DEERGEGPAPGSDTDPGRSDGDTDSVNWVADVEITGTPPYGGTAVVGRTE
      EERNILHADSNGYNLDPVQPSHSPTENSKGQSPBKRKSGVNVNPTNRASETP
      TMFVLDLGYOPGSGDSIPITALVGGGTRLDQKQYVRKSGVNVNPTNRASETP
      EIRYKRRFNSBILCALMGVNLVGTENGMLDRLSGQGVGVLIGRRRQOWDVE
      GINLITISGRNKLRYVLSLWENKLIHNDPEVEKQGTWVDMGCGHRYVRYKE
      RIKRLVIALKSSVEYVYAMAPRYKRFAPAFSFDLPRLPLVDTVEBQRLKITYGS
      SAGFHAVDVDSNGSYDIYIPVHIQSOLTPHALIFLPPTDGMELLCEDREKVVNTG
      RIKDVLQWQEMPTSVAYICSNQIMGKGAIRIRVEVTEGHLGDVFMHAKRAQKLEL
      CERNDKVFASVRSQSSQVYFMTLNRCINMW"
  ORIGIN
    1..3888
      AB035698 length: 3888 April 15, 2005 16:45 Type: N Check: 9874
      ab035698
  Alignment Scores:
    Pred. No.: 0 length: 3888
    Score: 5057.77 Matches: 624
    Percent Similarity: 21.51% Conservative: 0
    Best Local Similarity: 21.51% Mismatches: 257
    Query Match: 47.14% Indels: 2276
    DB: 1 Gaps: 148
  US-10-029-115-2 (1-1312) x ab035698 (1-3888)
  QY 6 ProAlaArgSerLeuAspAspLeuSerAla-LeuArgAspProAlaGlyIlePh 25
  Db 3885 CCGG--T--TCAT--GAT-----GCAGTTACGG-----TT 3862

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QY 25 e-GluValMetGluValValGluAsnGlyThrTyGly-----GluValTyrySeg 42
Db 3861 CAGAGTC-AT-GAGTA-----ACCT-----GGCTGCTGCCCCAGCA--G--C--G 3823
QY 42 IY--Arg-----His--Valys-----ThrGlyGln-----Leu-Ala-----A 52
Db 3822 GACTAGGCGCAAAAACACCTGTCTCAT-TCCGCTCACA--CAGAACTTGAACCTCTGAG 3767
QY 52 IallIelysVal-----Met--Asp---ValThrGuaAspGluGluGluIlelysgln 68
Db 3766 CTC-----GTTTGTCAGTAAAGACCCCGTC-----3742
QY 69 GluIleAsnMet-----LeuylslyrTySerHisArg-----AsnIleAlaThr 84
Db 3741 GAGGT-GG-CC-CGCTC-----CACAGAGCGGAGTCTCAATG-----3708
QY 85 TyTyGlyAlaPheIlelylsySerProProGlyAsnAspAspGln-----Leu-Tyr 102
Db 3707 -----GCTTTC-----TCACCC-----CAGCCATTATCTGG 3681
QY 103 LeuValMetGluPhe--CysGlyAla-----Gly-----SerValT 114
Db 3680 TTG-----GAGCA-GATGTAG-GCCACAGAGTAGGATCTCCCCCAGTCGAGC--A 3632
QY 114 hrAspLeuValysAsnThrlysgly-AsnAlaLeuylsGluAspCysIleAla--TyrI 133
Db 3631 CC-----ACATC-CT-TAATGA-----TGC--GCCGTCAG 3605
QY 133 IeCys--ArgGluIleLeuArgGlyLeuAlaHis-----Leu--His-Ala-His 147
Db 3604 --TGTTGAGCT-----AGA-----CACCTCGTCTCTGTAGCAGAGCAGCT 3565
QY 148 LysValIleHis--ArgAspIlelysglyGlnAsnValLeuLeuThrGluAsnAlaGluV 167
Db 3564 C--T--C--CAGCCGTCG--GTG--TTGGG-GAG--GAA--3538
QY 167 allIelysValAspPhe-----GlyVal--Ser-AlaGlnLeuAspArgThrValGly 183
Db 3537 -----GATGA-TGGCATGGGGCGTGAITCGCT--CTGGAT-----GTGC--3501
QY 184 ArgArgAsnThrPheIleGlyThrProTyTyPheAlaProGluValIleAlaCysAsp 203
Db 3500 -----ACA-----GGG-----AGT--A--GAGTCTATAC-TGTT--3475
QY 204 GluAsnProAspAlaThrTyArgSerArgSerAspIle-----Tyr-----Serie 219
Db 3474 -----CCC-----CGAGT-CGACATCCACAGCATGGAAGCCAGC--3442
QY 219 uGlyIleThr--AlaIleGluMetAla--GluGly--AlaProProLeu-Cys---234
Db 3441 -----ACTGAGCCATAG--ATGAC-CTTAAGCC-GCTGCCCTCTCTATGTCAG 3393
QY 235 --AspMetHisProMetArg-----Ala-----Leu-----242
Db 3392 TCGACCA-GC-----AGAGGCGGTGGGAGGTGGCAAGAAGCTTGAAGCCATGA 3341
QY 243 -Phe-----LeuIle--ProArgAsnPro--ProProArgLeuylsSerlylsys 257
Db 3340 ATTTGTGTAGGATTGGG-GGCCAGGCA-TA-CACCTCCAGC-----AGC-----3296
QY 258 TrpSerlylsPheIleAspPheIleAsp-----ThrCys-----Leu--Ilelys--272
Db 3295 ---TCTT--GA-GG-GC-GAT-----GACCAGAACTTA-ATCCGCTGTATTTC-ACA 3252
QY 273 --ThrTyLeuSer--Arg-----Pro-----ProThrGlu-----Gln--LeuLeu 285
Db 3251 ACACGGT-----AGTCCCGCAGCCCTCATGCCCCCAGAGT-GGTCAGGCCCTGCTTC- 3198
QY 285 sPhe-Pro-Phe-----IleArgAspGln-----ProThrGlu--Arg-GlnVal 298
Db 3197 -TTCTCCACTCTCGGCTATTG--TG-CAGAACTTGTTCG--GAGCCAGGACAGGTA 3145

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QY 299 ArgIleGlnLeuLysAspHisValLeuArgSerArgLysArgGlyGluLysGluGln 318
DB 3144 ---ATA-----CAC-----CCAGTTT-GT----- 3128
QY 319 ThrGluTyrGluTyrSerGly-SerGluGluGln--AspAspSerHisGlyGluGln 337
DB 3127 ---TCCTT-TTCCCT-GAGAT-GGTGAT-----GAGCA-GG 3099
QY 337 Y-Glu-ProSerSer-IleMetAsnValProGlyGluSerThrLeu---ArgArgGlu 354
DB 3098 TTGAGCGCCCTCCAGCAGATCCA-----TCTG--CTGAGAGCGTCCG-- 3060
QY 355 PheLeuArgLeuGlnGlnGlnLeuLysSerAsnSerGlu-----AlaLeuLysGln 372
DB 3059 ---CGCC--CAAT--GAG-----TCAT-ACACCTTGCCCTGCC-CA--- 3027
QY 372 ngInGlnLeu---GlnGlnGln-GlnGlnArgAsp-ProGluAlaHisValLeuHisL 390
DB 3026 ---CTTGGGTCCAGACA-TCAGCC-CGTTT-TCGGT--GCC----- 2992
QY 390 euLeuHisValn-Arg-----GlnArg-----ArgIle---GluGluGlnLys 402
DB 2991 ---CACGACGAGGTTCACCCCCAAGCGCTGCACAGAGGATCTCGAGATT- 2944
QY 403 GluGluArg-----Arg-----Arg-----ValGluGluGlnArg- 413
DB 2943 GAAT--CGCTTTCTTACTTCGGATCTCAGGGGTCTCCTGTGG-CC-----CGGG 2894
QY 414 ---Arg-----Glu-----ArgGluGlnArgLysLeuGln 422
DB 2893 TGTGTGGGATTTCAGTTGACACAGAACCCCTTCCTCAGT-----CGTA--CTGAG 2842
QY 423 ---GluLysGluGlnGlnArg-----Arg-LeuGluAsp---M 433
DB 2841 CTGTGTGAGC-----CGAGTCCCTCTCCACCCACTAAGGGCTGT--GATGGGGA 2795
QY 433 eGlnAla-----LeuArgArgGluGluArgGlnArgGlnArg-ArgGluGln 449
DB 2794 TGCT-GT-CCCCACTGCTC-----CAGGCTGG-TGAT--CC- 2762
QY 450 GluTyrLysArgLysGlnLeuGluGlnGln---ArgGlnSerGluArg-LeuGlnArg 468
DB 2761 CT-----AGATC-CA-----CAACATCGT-----GAACGAGCTC- 2733
QY 468 InLeuGlnGlnGlnHisVala--TyrLeuLysSerLeuGlnGlnGlnGlnGln 487
DB 2732 ---TTGC--CAGGG-----GCCCTTAC----- 2716
QY 487 nLeuGlnLysGlnGlnGlnGlnLeuLeuProGlyAspArgLys--ProLeu 504
DB 2715 ---CAG-----CAG-----CCCA--CG-AGACT-GGTAGTCACCACTC 2688
QY 505 TyrHisTyrGlyArgGlyMetAsnProAlaAspLysProAla-Tyr-----Ala-----A 521
DB 2687 C--CATCC-TT-CAGAGGT--GG-----GCTTGGCCCTTCTGCTGTTCTC 2650
QY 521 rg-----Glu-----ValGluArgThrArg----- 528
DB 2649 GGTGGGTAGGTGGCTGGCTGACACACGTC-----AGGC--AGGTTTGTATACCATG 2598
QY 529 ---MetAsnLysGlnGlnAsnSer--ProLeu-----AlaLysSerLysP 542
DB 2597 CTGTACAGCACTG-----CAGCAGGT-TCGCTCTCTTCAGGGGTGCGCT- 2555
QY 542 roGlySerThr--GlyProGluProProLysProGln-----AlaSerProGlyProP 559
DB 2554 ---GAGAC-ACCATGTGTG-----CCGCCC--CCGTA-TGGGGGCT-----GGGT--CCC 2515
QY 560 GlyPro-Leu-SerGlnThr-----ProPrometGln---ArgPro---ValGluP 574
DB 2514 GGTGA-TCTCCCTCG--ACGTGTGTGACACACC-ATGGT-GCTGACGCTG-TCTGAT- 2465
QY 574 roGlnGluGlyProHisLysSerLeuGlnAspGlnProThrArgAsn---Leu-Ala--- 591

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DB 2464 ---CCCCATC--G--CTGC--G--G--CCCC-AGGGG-TATCTGTGCTCCC 2428
QY 592 ---AlaPheProAla-SerHisAspProAspProAlaIleProAla---Pro-ThrAl 608
DB 2427 CTGTCTGG-CCCGCTTCG-----CCTT--CCT--CCTGG-TGCTCTCACTGC 2384
QY 608 a-----Thr-ProSerAlaArg-GlyAlaValIleArgGlnAsnSerAspProThSerG 626
DB 2383 TTTCACCTTCCT-----CGCTGGA-----CGAC--G--AGT-----AGT-- 2354
QY 626 uGlyProGly--ProSerProAsnProAlaTyrValArgProAsnGlnAlaPro- 645
DB 2353 ---CCATG-GCCTTCT-----TGGG--AGG-----CCGA 2331
QY 646 ---ProLysValProGln---ArgThrSer--SerIleAlaThrAlaLeuAsnThr- 661
DB 2330 GGGGCTTC--GTG--CAGAGTCCG--TCTTTGAGC-----AACCAAA 2294
QY 662 SerGlyAlaGlyLysArgProAlaGlnAlaVal--ArgAla--ArgProArgSerAs 680
DB 2293 AGTCT-GGGGGC-----CGGCTG--GCCGTAGCGGTG-GTGT--CGG----- 2255
QY 680 nSerAlaTyrGlnIleTyrLeu-Gln---Arg---ArgAlaGlu---Arg-----G 694
DB 2254 ---GCTTGGC--TT-TATTC-CCAGGGGAGAGACACAGGG--GAGCTGTCCGTTTGAG 2205
QY 694 ly-ThrProLysProPro---Gly-Pro--ProAla---GlnProPro---GlyPro 708
DB 2204 GAGACT-----CCACAGCGGTTCGCTCCACT-GAGCCAGCGCTG-GGAGGT- 2159
QY 709 ProAlaHisSerSerAsnProAspLeuArg-ArgSerAspProGlyTyrGluArg- 726
DB 2158 ---GCC-----CGTGA------GCTGA-AGGACGCT 2134
QY 727 -SerAspSerValLeuProAlaSerHisGlyHisLeuProGlnAlaGly--Ser--Leu 744
DB 2133 GTCCG--AGCGTT---CCC--AGC-----CAG--GGTGGCTCTCTCTCG 2100
QY 745 GluArgAsnArg-Val-----Gly--AlaSerSerLysLeu---AspSerSer- 758
DB 2099 ---AGGT--CGGGGTACTGCGACGAGCTGCT--G--GG-CTGGCCGGAGCC-TCCGG 2051
QY 759 --Pro--ValLeu-----SerProGlyAsnLysValLysProAsp--AspHisAspSer- 774
DB 2050 CCCCACGTGTGTTAAGGCACT--GGC-----GATGATG--AGGTCT 2011
QY 775 ---Arg-Pro-----GlyArgProAlaAspPheValLeuLysGluArgThr---L 790
DB 2010 CTGAGGACACTTGGGTGGG--CTTC-----GTAT-CTGG--G--CGAACCCAGCG 1966
QY 790 eu--AspGluAlaProArg-----Pro--ProLysValAlaMetAspTyrSerSer 805
DB 1965 TGGGGGATT-----CGGGCTGGGGCGAGGTCT----- 1938
QY 806 SerSerGluGluValGluSerSerGlu-----AspAspGluGluGluGluGlyG 823
DB 1937 ---TCA-----GAGGTGG--GG-TCTGAATTCTGGCGGATGACAG-CT----- 1902
QY 823 lyPro--AlaGluLysSerArgAspThrProGly-----Gly-ArgSerAsp---GlyA 839
DB 1901 ---CTTCGGGCACT--GGG--CGT-----GGCAGTGGGTGGCGG--GATGGACAGG- 1860
QY 839 sPThrAspSer--ValSerThrMetValValHisAspValGlu-----GluIleThrGly 856
DB 1859 ---TCGGGGTC-----ATGG-----GAGGCTGGGAAG- 1835
QY 857 ThrGlnPro-----ProTyr--Gly---Gly---GlyThr----- 865
DB 1834 ---CAGCCAGGTTTCGGGTGGGCTGTGCTGC--AGGACCTGGAGATCGGATACAGTCT 1779
QY 866 ---MetValValGln-----Arg-----ThrProGluGluGluArgAsnLeuLeuH 880

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Search completed: April 19, 2005, 10:18:37
Job time : 48 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2005, 10:05:37 ; Search time 7 Seconds

(without alignments)
1.457 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 9301
Sequence: 1 MGDPARSLDDIDLSALRD.....SGSSQVYFMTLRNCIMNMW 1312

Scoring table: BLOSUM30

Xgapop 0.1, Xgapext 0.0
Ygapop 0.1, Ygapext 0.0
Fgapop 0.1, Fgapext 0.0
Delop 0.1, Delext 0.0

Searched: 1 seqs, 3888 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ _p2n.model -DEV=soft -Q=US10029115.pep -DB=ab035698.seq
-SUFFIX=ptc -OUT=aai.res -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum30 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORML-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO XLPXY
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=0.1 -XGAPEXT=0 -FGAPOP=0.1
-FGAPEXT=0 -YGAPOP=0.1 -YGAPEXT=0 -DELOP=0.1 -DELEXT=0

Database : ab035698.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	9016.2	96.9	3888	1	ab035698 TOIG of: ab035698
2	4928.97	53.0	3888	1	ab035698 TOIG of: ab035698

ALIGNMENTS

RESULT 1
ab035698
TOIG of: ab035698 check: 9874 from: 1 to: 3888

LOCUS AB035698 3888 bp mRNA linear PRI 18-APR-2000
DEFINITION Homo sapiens mRNA for Mischapen/NIK-related kinase MINK-1, complete cds.
ACCESSION AB035698
VERSION AB035698.1 GI:6970477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases)

AUTHORS

Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Nimomiya-Tanji, J. and Kusumi, A.
Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development

TITLE

JOURNAL FEBS Lett. 469 (1), 19-23 (2000)

JOURNAL

MEDLINE 20175403

REFERENCE

2 (bases 1 to 3888)

AUTHORS

Dan, I., Watanabe, N.M. and Kusumi, A.

JOURNAL

Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane Organizer Project: 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dange@lo.nagoya-u.ac.jp, Tel: 81-52-789-2497, Fax: 81-52-789-2968)

FEATURES

Location/Qualifiers

source

1. 3888

gene

1. 3888

CDS

1. 3888

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US-10-029-115-2 (1-1312) x ab0355698 (1-3888)

QY 1 MetGlyAspProAlaProAlaArgSerLeuAspAsp1LeuSerAlaLeuArgAsp 20
 Db 1 ATGGGGAGACCCACCCCGCCCGAGCTGGAGCACTGCACCTGCTCCGCGCGGAG 60
 QY 21 ProAlaGly1LeuPheGluLeuValGluValAlaGlyAsnGlyThrTyrGlyGluValTyr 40
 Db 61 CTGGCTGGAGCTTTTGAAGCTTGTGGAGGTGTGTGGCAATGAACTTACGAGAGGTGTAC 120
 QY 41 LysGlyArgHisValIleYsthrGlyGlnLeuAlaAlaIleYsthrValIleAspValIthrglu 60
 Db 121 AAGGGTCGGCATGTCAAGACGGGGAGCTGGCTGCATCAAGGTCAATGATGCACGAG 180
 QY 61 AspGluGluGluGluIleYsthrGlnGluIleAsnMetLeuIleYsthrSerHisIleArg 80
 Db 181 GAGGAGAGAGAGAGATCAAAACAGAGATCAACATGCTGAAAAAGTACTTCAACACCGC 240
 QY 81 AsnIleAlaThrTyrTyrGlyAlaPheIleYsthrSerProProGlyAsnAspAspGln 100
 Db 241 AACATGGCCCTCACTACGAGAGCTTCTATCAAGAAAGCCCGCGGAAACGATGACACG 300
 QY 101 LeuTyrLeuValMetGluPheCysGlyAlaGlySerValThrAspLeuValIleYsthr 120
 Db 301 CTCTGGCTGGTGAATGGAGTTCTGTGGTGTGTGCTGAGTCACTGCTGTAAGAACACA 360
 QY 121 LysGlyAsnAlaLeuIleYsthrAspCysIleAlaTyrIleCysArgGluIleLeuArgGly 140
 Db 361 AAAGGCAACCCCTGGAAGGAGAGCTGTATGCTATCTGCAAGGAGATCTTCAGGGGT 420
 QY 141 LeuAlaHisLeuHisIleHisIleYsthrValIleHisIleAspAspIleYsthrGlnAsnValIle 160
 Db 421 CTGGCCCATTTCCATGCTCCCAAGGTGATCATCGACATCAAGGGGCAATGTGTCTG 480
 QY 161 LeuThrGluAsnAlaGluValIleYsthrValIleAspPheGlyValIleSerAlaGlnLeuAspArg 180
 Db 481 CTGACAGAGATGCTGAGGTCAAGCTAGTGAATTTGGGGTGAAGTGTCACTGACCGC 540
 QY 181 ThrValGlyArgArgAsnThrPheIleGlyThrProTyrTyrMetAlaProGluValIle 200
 Db 541 ACCGTGGGCGAGAGCACTTTCATTTGGGACTCCCTCACTGAGATGGTCTCAGAGGTATC 600
 QY 201 AlaCysAspGluAsnProAspAlaThrTyrAspTyrArgSerAspIleTyrSerLeuGly 220
 Db 601 GCTGTGATGAGAACCTGTATGCCACTATGATTAACAGAGTATTTGTGTCTTACGA 660
 QY 221 IleThrAlaIleGluMetAlaGluIleValProProLeuCysAspMetHisProMetArg 240
 Db 661 ATCAGAGCCATCGAGATGGCAGAGGGAGCCCGCTGTGTGATGACATGCCATCGCA 720
 QY 241 AlaLeuPheLeuIleProArgAsnProProProArgLeuIleYsthrIleYsthrSerIle 260
 Db 721 GCCCTTCTCTCACTTCTCTCGGAACCTCTCCGCCAGGCTCAAGTCCAAAGAGTGTCTAAG 780
 QY 261 LysPheIleAspPheIleAspThrCysIleIleYsthrTyrLeuSerArgProProThr 280
 Db 781 AAGTTATTTGACTTCTTGAACATGTTCTCATCAAGACTTAACCTGAGCCGCCCAACCA 840
 QY 281 GluGlnLeuLeuIleYsthrPheIleArgAspGlnProThrGluArgGlnValArgIle 300
 Db 841 GAGCAGACTACTGAAGTTTCCCTTCATCCGGGACCAAGCCAGCGGAGCGGTCCGATC 900
 QY 301 GlnLeuLeuYsthrHisIleAspArgSerArgIleYsthrArgGlyIleYsthrGlu 320
 Db 901 CAGCTTAAGGACCACTTGAACCATCCCGAAGAGAGGGGTGAGAAAGGAGGACAGAA 960
 QY 321 TyrGluTyrSerGlySerGluGluGluAspAspSerHisIleGlyGluGluGluProSer 340
 Db 961 TATGATGACGCGGAGCGAGAGAGATGACGCAATGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 341 SerIleMetAsnValProGlyGluSerThrLeuArgArgGluPheLeuArgLeuGln 360

Db 1021 TCCATCATGAGAGTGCCTGGAGAGTGCATCAAGCCCGGAGATTTCTCCGGCTCCAGCAG 1080
 QY 361 GluAsnLysSerAsnSerGlnAlaLeuIleYsthrGlnGlnGlnGlnGlnGlnGln 1100
 Db 1081 GAAATTAAGACCACTCAAGAGCTTTAAACACAGACAGACAGCTGACAGACAGCAG 1140
 QY 381 ArgAspProGluAlaHisIleYsthrHisIleLeuHisIleGlnArgGlnArgIleGlu 1200
 Db 1141 CGAGACCCGAGGACACATCAAAACCTGTGACACCAAGGAGAGGAGGAGGAGGAGGAG 1260
 QY 401 GlnLysGluGluArgArgArgValGluGluGlnGlnGlnGlnGlnGlnGlnGlnGln 1280
 Db 1201 CAG 1300
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 QY 521 ArgGluValGlnGluArgThrArgMetAsnLysGlnGlnAsnSerProLeuAlaYsthr 1540
 Db 1561 CGAGAGTGAAG 1560
 QY 541 LysProGluSerThrGlyProGluProProIleProGlnAlaSerProGluProProGly 1580
 Db 1621 AAGCCAGGAG 1600
 QY 561 ProLeuSerGlnThrProProMetGlnArgProValGluProGlnGluIleProHisIle 1620
 Db 1681 CCCCTTCCAGACTCTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1640
 QY 580 ----- 580
 Db 1741 AGCCTGGTGACACCGGAGTCCCATGAAGCCATATGACAGCACTGTACCCCGATCCAG 1800
 QY 581 SerLeuGlnAspGlnProThrArgAsnLeuAlaIlePheProAlaSerHisAspProAsp 1820
 Db 1801 TCCCTGAG 1840
 QY 601 ProAlaIleProAlaProThrAlaThrProSerAlaArgGlyAlaValIleArgGlnAsn 1860
 Db 1861 CCGGCATCCCGGACCACTGCGACGCGCAGGCGCGAGAGGTCTCATCCGCCAGAAAT 1920
 QY 621 SerAspProThrSerGluGlyProGlyProSerProAsnProProAlaTyrValArgPro 1940
 Db 1921 TCAGACCCCACTGTAAG 1960
 QY 641 AspAsnGluAlaProProLysValProGlnArgThrSerSerIleAlaThrAlaLeuAsn 1980
 Db 1981 GATTAAG 2000
 QY 661 ThrSerGlyAlaGlyGlySerArgProAlaGlnAlaValArgAlaArgProArgSerAsn 2020
 Db 2041 A-----CCAG----- 2045
 QY 681 SerAlaTyrGlnIleTyrLeuGlnArgArgAla-GluArgGlyThrProLysProProGlu 2060
 Db 2046 -----TGGG-----GCCGAG-----GGT-----CCCGG 2064

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QY 700 yProProAlaGlnProProGly---Pro--ProAsnAlaSerSerAnProAspLeuArg 718
Db 2065 C-----CAGC--CGAGGAGCTCGGCCAGT-----NAACCCGAGCTCAGG 2103
QY 719 ArgSerAspProGlyTTrpGluArgSerAspSerValLeuProAlaSerHisGlyHisLeu 738
Db 2104 AGAGAGGAGCCCTGGCTGGAGAGCTCGAGAGCTTCCAGCCTTCAAGCGGAGCACTTC 2163
QY 739 ProGlnAlaGlySerLeuGluArgAsnArgValGlyAlaSerSerLeuLeu-AspSerSe 758
Db 2164 CCCAGGCTGGCTCACTGAGCGGAAACCCGCTGGAGCTCTCTCCCAACCC-GGACGCTC 2222
QY 758 xProAlaLeuSerProGlyAsnAlaValAlaProAspAspHisArgSerArgProGlyArg 778
Db 2223 CCTGTGCTCTCCCTCGGAAATTAAGCCAGACCCGAGCAGCAGCTCAGCGGCGAGGCGG 2282
QY 778 gProAlaAspPheValLeuLeuLeuArgTrpLeuAspGluAlaProArgProGly 798
Db 2283 GCGCCGAGACTTGTGTCTGTAAGAGCGGACTCTGAGCGAGGCCCTCGGCTTCCAA 2342
QY 798 sAlaValaMetAspTyrSerSerSerSerGluGluValGluSerSerGluAspAspGlu 818
Db 2343 GAAGGCGCATGAGACTCTCTCTCCAGCGAGGAGGTGGAAGAGCAGTGAAGCAGCAGCA 2402
QY 818 uGluGluGlyGluGlyProAlaGluGlySerArgAspTrpProGlyGlyArgSerAspG 838
Db 2403 GGAAGGCGGAGGCGGCGGCGAGGAGGAGCAGAGTACCCCTGGGGGCGCGAGCATGG 2462
QY 838 yAspTrpAspSerValSerTrpMetValValHisAspValGluGluLeuLeuHisGly 858
Db 2463 GGATACAGACAGCTGACAGCATGGTGTCCAGCAGCTGAGAGAGATACCGGAGCCCA 2522
QY 858 nProProTyrGlyGlyGlyThrMetValValGlnArgTrpProGluGluArgAsnLe 878
Db 2523 GCGCCCATACGGGGGCGGCGACCATGGTGTCCAGCGCACCCCTGAAGAGAGCGGAACT 2582
QY 878 uLeuHisAlaAspSerAspGlyTyrTrpTrpLeuLeuProAspValValGlnProSerHis 898
Db 2583 GCTGATGCTGACAGCATGGGTGACCAACCTGCTGACGTGTCCAGCCAGCCAGCTC 2642
QY 898 rProTrpGluAsnSerLeuGlyGlnSerProProSerLeuAspGlySerGlyAspTyrG 918
Db 2643 ACCACCGGAGAACAGCAAGGCGCAAGCCCTCTGAAGAGTGGAGAGTGTGACTACCA 2702
QY 918 nSerArgGlyLeuValValAlaProGlyLysSerSerPheTrpMetPheValAspLeu 938
Db 2703 GTCTGCTGGGCTGTGTAAGGCCCTGTGCAAGAGCTGTTCACGATGTTGTGATCTAG 2762
QY 938 yLeuTyrGlnProGlyGlySerGlyAspSerLeuLeuLeuLeuValGlyGlyG 958
Db 2763 GATCTACACGAGCTGTGAGGCGAGTGGGAGCATCCCATCAAGAGCCCTGTGGTGGAGA 2822
QY 958 uGlyThrArgLeuAspGlnLeuGlnTrpAspValArgLeuGlySerValValAsnValAs 978
Db 2823 GGGCACTCGGCTCGACCACTGACATGACAGTGAAGAGGTTCTGTGTCACACTGAA 2882
QY 978 nProTrpAsnTrpArgAlaHisSerGlyTrpProGluLeuArgLysTyrLysLeuArg 998
Db 2883 TCCCAACCAACACCCGGGCGGAGTGAAGCCCTGTGATCCGGAAGTACAGAGAGGAT 2942
QY 998 eAsnSerGluLeuLeuCyAlaAlaLeuTrpGlyValAlaLeuLeuValGlyThrGluAs 1018
Db 2943 CAACCTCCGAGATCTCTGTGAGCCCTTTGGGGGGGTCAACCTGTGTGGGCGAGAGAA 3002
QY 1018 nGlyLeuMetLeuLeuAspArgSerGlyGlnGlyLysValTyrGlyLeuLeuGlyArg 1038
Db 3003 CGGGCTGATGTTCTGTGAGCGAGTGGGAGGCGGAGGAGGTGATGACTATTGGGCGGG 3062
QY 1038 gArgPheGlnGlnMetAspValLeuGluGlyLeuAsnLeuLeuLeuHisSerGlyLys 1058
Db 3063 ACGCTTCCAGAGATGATGTCTGTGAGGGGCTCAACCTGTCTCATCATCATCAAGGAA 3122

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QY 1058 sArgAsnLysLeuArgValTyrTyrLeuSerTrpLeuArgAsnLysLeuHisAsnAs 1078
Db 3123 AAGAAACAAATCGCGGGTATATACCTGTCCGGTCCGGAAACAAGATTCTCACAATGA 3182
QY 1078 rProGluValGluLysLysGlnGlyTTrpTrpTrpValGlyAspMetGluGlyCyGlyHis 1098
Db 3183 CCCAAGAGTGGAGAAAGAGAGGCGTGGACCAACCTGTGGGGGAGCATGAGGCGTGGGGA 3242
QY 1098 sTrpArgValValLysTyrGluArgGlyLeuPheLeuValLeuAlaLeuLysSerVal 1118
Db 3243 CTACCGTGTGTGAATACGAGCGGATTAAGTTCCTGTGCATCGCCCTCAAGAGCTCC 3302
QY 1118 lGluValTyrAlaTrpAlaProLysProTyrHisLysPheMetAlaPheLysSerPheAl 1138
Db 3303 GGAGGTGATGCTGTGGGCGCCCAACCTTACCAAAATTCAAGGCTTCAATCTTTC 3362
QY 1138 sAspLeuProHisArgProLeuLeuValAspLeuTrpValGluGluGlyGlnArgLeu 1158
Db 3363 CGACCTCCCGCACCCGCTGTCTGTGAGCTGACAGTGAAGAGAGGAGGCGAGCGCTCA 3422
QY 1158 sValLeuTyrGlySerSerAlaGlyPheHisAlaValAspValAspSerGlyAsnSer 1178
Db 3423 GGTCACTATGCTCTCAGTGTGCTGTCCATGTGTGATGTGCACTGGGGAACAGCTA 3482
QY 1178 rAspLeuTyrTrpLeuProValHisLeuGlnSerGlnLeuTrpProHisAlaLeuLeu 1198
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QY 1198 uProAsnTrpAspGlyMetGluMetLeuLeuCyArgTrpGluAspGluGlyValTyrValAs 1218
Db 3543 CCCCAACACCGAGCATGAGATGCTGTGTGACAGAGAGAGGAGGTCTACGTCA 3602
QY 1218 nThrTyrGlyArgLeuLeuLeuValValLeuGlnTrpGlyGluMetProTrpSer 1238
Db 3603 CACGTACCGGCGCATTAAGATGTGTGTGCAAGTGGGGGAGATGCTTCACTTCTGT 3662
QY 1238 lAlaTyrLeuCySerAsnGlnLeuMetGlyTTrpGlyGluValAlaLeuLeuAsp 1258
Db 3663 GCGCTTACATCTGCTTCAACCATATATGGCTGTGGGTGAGAAAGCATTAAGATCCGCTC 3722
QY 1258 rValGluThrGlyHisLeuAspGlyValPheMetHisLysArgAlaGlnArgLeuLys 1278
Db 3723 TGTGAGAGCGGCGCACCTCGACGCGGCTCTTATGACAAACAGACTCAGAGGCTCAAGTT 3782
QY 1278 eLeuCyGluTrpArgAsnAspLysValPhePheAlaSerValArgSerGlyGlySerSer 1298
Db 3783 CCTGTGTAGCGGAATGACAAAGTGTGTTTTCCTCAAGTCCGCTGTGGGGGCGAGCA 3842
QY 1298 nValTyrPheMetThrLeuAsnArgAsnCyAlaLeuLeuLeuLeuLeuLeu 1312
Db 3843 AGTTTACTTCATGACTGTGAACCGTACATGCAATGAATGG 3885

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RESULT 2
 AB035698/c
 TOIG OF: ab035698 check: 9874 from: 1 to: 3888

LOCUS AB035698 3888 bp mRNA linear PRI 18-APR-2000
 DEFINITION Homo sapiens mRNA for Mismatch/NIK-related kinase MINK-1, complete cds.
 ACCESSION AB035698
 VERSION AB035698.1 GI:6970477
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (sites)
 REFERENCE
 Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Matsumoto, K., Niinomiya-Tsuiji, J., and Kusumi, A.
 Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development.


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Db      1664 GAGCCCTGGGG--GATGGG--GAGC--T--CAGCCCCCGCTGCTGCTTCTT- 1615
Qy      925 AlaPro--GlyIysSerSerPhe-Thr-MetPheValAspLeuGlyIle-----Ty 940
Db      1614 GG-CGAGGAGAG--TTCTGCTGCTTGTTCATC--CTT--GTTCTCTTCTA 1568
Qy      940 r--Gln--ProGly-Gly-----SerGlyAspSerIle-----Pro--Ile----- 951
Db      1567 CCTCTCGGGGCCAGGCTGGTGTGTGACGGG--ATTCAATGCCCCGACATAATAGT 1514
Qy      952 Thr-AlaLeu--Val--Gly-Gly-----Glu----- 958
Db      1513 ACAGGGGCTTCTCTGCCCCAGGAGAGCTGCTGCTGCTGCTTCTGTAAGCTGCTGCT 1454
Qy      959 -----GlyThr-----Arg-----LeuAspGlnLeuGln-T 967
Db      1453 GCTGTTGCTGCTGCTGCTGAGGAGACTTGAAGTAGAGATGCTCTGCTG--CAGCTGCTCT 1397
Qy      967 yr-AspVal-----Arg-----Lys--GlySer--ValVal-----A 976
Db      1396 GAGAGCTTGTGATGCTGCGCTGCTCTCCAGCTGCTTCCGCTTGTATCTGCTGCTGGCT 1337
Qy      976 snValAsnPro--ThrsAnthr-----ArgAla--His-Ser--Glu----- 987
Db      1336 CCGCGCTG-CGCGCGCTCTCTCTCCCGCGAGAGCTGCAATGCTCTCCAGCCGCGCTGC 1278
Qy      988 -----ThrPro-GluIle-----ArgLys-----Tyr-----Lys 995
Db      1277 TGTCTCTTCTCTGCAAGCTTCCGCTGCTCCGCTCCGCGCTGCTGCTCTCAAGCGG 1218
Qy      996 LysArg-----PheAsn--SerGluIleLeuCys--AlaAlaLeuTrp-----GlyV 1010
Db      1217 CGCGCGCTCTCTCTCTGCTCTGCTCT--CTATGCGCGCGCTCGC--TGGAGCAGCAGGTG 1165
Qy      1010 aLAsnLeuLeuValGlyThrGluAsnGlyLeu-MetLeuLeuAspArgSerGlyGln-- 1028
Db      1164 TTTCG-ATGT--GTGCC-TCCG--GCTCTGCTGCTGCTGCT--T--GCTG--CAGCTG 1120
Qy      1029 -----Gly-----Lys-----Val-----Tyr-----GlyLeuIleGly-- 1036
Db      1119 CTGCTGCTGTTTAAAGCCTTGAAGTTCCTTATTTCTGCTGGA--GCCGAGAAA 1063
Qy      1037 ---ArgArgArg-----PheGln--Gln-MetAspValLeuGln--Gly-LeuAs 1050
Db      1062 CTCGCGCGGTAGAGTGAAGCTCCAGGACAGTTCAATG--GAGCTTGGCTCTC-- 1010
Qy      1050 nLeu--Leu-----IleThrIle-SerGlyLysArgAsnLysLeuArgValTyr-- 1065
Db      1009 -CTTCTCTCTCCATGAGCTGTC--ATCTTCT--CTTCCG--TGGCGCTG-TACTCA 963
Qy      1066 Tyr-LeuSerTrpLeuArgAsnLysIleLeu--HisAsnAspPro-----Glu--Val 1081
Db      962 TATTCGTCTC--CTC-----TTTCTCAC-----CCCGCTTTTCCGGGATC 923
Qy      1082 GlnLysLysGln--Gly-----Tyr-----ThrValGly----- 1091
Db      922 G--G--T--CAATGTGCTCTTAAGCTGAGTGGAGACTGCGCTCGTGGGCTGGTCCC 869
Qy      1092 -AspMetGluGly-----Cys-----GlyHisTyr-Arg-----Val-ValL 1103
Db      868 GGAAT--GAAGGAAACTTCAGTAGCTGCTGCTGGG--TGGCGGCTCCAGGTAAGTTC- 816
Qy      1103 yETyrGlu-Arg-----Ile-----Lys-----PheLeu-ValIleAlaLeuLysse 1116
Db      815 --TTGAT-GAGACATGTGTCAATGAAGTCAATGAATCTTTAGAC--AC 771
Qy      1116 rSerValGluValTyr-----AlaTrpAla-----Pro-----LysPro--T 1128
Db      770 TTCT-----TGAGCTTGAAGCTTGGGAGAGGTTCCGAGAAATGAGAGAG--GCG 721
Qy      1128 yr-HisLys-Phe-MetAlaPheLysSerPheAlaAspLeuProHisArg----- 1143
Db      720 TCCGATGG-GGTGCATG--TCA-----CACAGAGGGGGGGCTC 686

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Qy      1144 ProLeuLeuVal--Asp--LeuThrValGlu-GluGlyGlnArgLeu-----LysValIle 1160
Db      685 CCTCTGCC-ATCTCATGAGCTGG-ATTCTAGAGAC-CAAA--TATCACTCTCTGAATC 631
Qy      1161 Tyr-Gly-SerSerAlaGlyPhe-His-AlaValAspValAsp-SerGly----- 1175
Db      630 AT-AGGTGCATCA--GGTTCTCATCAAGGC-GAT--GACCTTGGAGCCATCCAG 579
Qy      1176 -----Asn--SerTyrAspIleTyrIlePro--ValHis-----IleGln- 1187
Db      578 TAGGAGTCCCATGAAGT-----GTTCTGCTGCTCCAGGCTGGCTTCACG 531
Qy      1188 -----Ser--Gln-Ile-Thr-----Pro--HisAlaIle-Ile-----P 1197
Db      530 TAGAGACTACACCCCAAAATCACTAGTACCTGACCTGACGATT--CTCTGACAGACAT 473
Qy      1197 heLeuPro-Asn--Thr--Asp-----GlyMetGluMet-----Leu- 1207
Db      472 TCTGCCCTTGATGTCTCATGATGATCAGCTGTGGGATGAGAGATGGCCAGACCCCTGA 413
Qy      1208 ---Leu-Cys--TyrGlu--Asp-----GluGlyVal-----TyrValAsn 1218
Db      412 GGAATCTCCCTGAGATATAG-CGATACAGTCTCTCTTCAAGGCGCTTGTGTGTG-- 356
Qy      1219 Thr-Tyr-Gly-----Arg-Ile-IleLysAspValValLeuG 1230
Db      355 TCTTTACAGAGTCAGTCACTGAACACAGACACAGAAATCCATC--ACCA--GC-C 305
Qy      1230 In--Trp-----Gly-----Glu-MetProHisSer--ValAl 1239
Db      304 AGAGCTGTCATGTCCTTCCCGGGGCTCTTCTTGAAGAGCTCGT--ACTAGTGGC 247
Qy      1239 aTyrIleCysSerAsnGlnIleMetGlyTyrGlyGlu-----LysAla-----Ile 1254
Db      246 GA--TGT--G--CGG-----TGGT--GAGACTACTTTTTCAGCAGATGTGATC 207
Qy      1255 ---Glu--Ile-----Arg--SerValGluThrGlyHis--LeuAspGly-- 1266
Db      206 TCTGTATTATCTCTTCCCTGCTGCTCTCGT--ACATC-CATGACCTTGAATGGCAGC 151
Qy      1267 -----ValPhe-Met-----HisLys--ArgAlaGlnArgLeuLys 1277
Db      150 CAGCTGCCCGTCTTGACATGCCGACCTTGTACACTT--GTCCGT-----AGG----- 104
Qy      1278 PheLeu-CysGluArg-----Asn-----AspLysValPhePheAlaSer---Y 1291
Db      103 TTCCA-TTGC--CGACCACTCCACAGACTCAAGATCCC-----AGCAGG 60
Qy      1291 aL-ArgSerGlyGlySerSerGlnValTyrPheMetThrLeuAsnArgAsnCysIleMet 1310
Db      59 TCCCGCAG-GCGGGA-----CAGTCC--ATGTCC--TCCAGGC--TGGCG-GCG 18
Qy      1311 --AsnTrp 1312
Db      17 GGGGCTGG 10

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Search completed: April 19, 2005, 10:06:28
 Job time : 50 secs

US-10-029-115-2 (1-1312) x ab035698 (1-3888)

QY 1 MeGlyAspProAlaProAlaArgSerLeuAspAsp11LeuSerAlaLeuAgaap 20
 Db 1 ATGGGGGACCCGCCCCCGCCAGCTGGAGCATGACCTGTCGCCCGCCGCGAGC 60
 QY 21 ProAlaGly11PheGluLeuValGluValValGlyAsnGlyThrTyrglyGluValTyf 40
 Db 61 CTTGCTGGGATCTTTTACGCTTGTGGAGGTGGTGGGMAATGMACTTACGGACAGGTGTAC 120
 QY 41 TyrglyArgHisValIleThrGlyGlnLeuAlaIleIleValMetAspValThrGlu 60
 Db 121 AAGGGTCGCATGTCAAGACGGGGCAGCTGGCTGCATCAAGGTCAATGATGACGAG 180
 QY 61 AapGluGluGluGluIleTyrglnGluIleAsnMetLeuIleTyrglnSerHisArg 80
 Db 181 GACGAGAGAGAAAGATCAAAACGAGATCAACATCTGAAAAAGTACTTCCACACCCG 240
 QY 81 AsnIleAlaThrTyrglyArgIlePheIleTyrglnSerProProGlyAsnAspAspGln 100
 Db 241 AACATGCGCACTTACTACGAGGCTTCAATCAAGAAAGCCCCCGGMAACATGACGAG 300
 QY 101 LeuTrpLeuValMetGluPheCysGlyAlaGlySerValThrAspLeuValIleAsnThr 120
 Db 301 CTCTGGCTGGTATGAGATTCTGTGGTGTGGTTCAGTGACTGACCTGGTAAAGAACACA 360
 QY 121 TyrglyAsnAlaLeuIleGluAspCylleAlaTyrlleCysArgGluIleLeuArgly 140
 Db 361 AAGGGCAAGCCCTGAAAGAGGACTGTATTCGCTTATTCGCGAGGAGATCTCCAGGGGT 420
 QY 141 LeuAlaHisGluHisIleHisIleValIleHisArgAspIleTyrglyGlnAsnValLeu 160
 Db 421 CTGGGCCATCTCATCTCCACAGGTGATTCATCGAGCATCAAGGGGCGAATGTGCTG 480
 QY 161 LeuThrGluAsnAlaGluValIleValLeuValAspPheGlyValSerAlaGlnLeuAspArg 180
 Db 481 CTGACAGAGAAATCTGAGGTCAAGCTAGTGGATTTGGGGTGAAGTCTCAGCTGAGACCG 540
 QY 181 ThrValGlyArgArgAsnThrPheIleGlyThrProTyrlleTrpMetAlaProGluValIle 200
 Db 541 ACCGTGGGAGACGGAACACTTTCATTTGGGACTCCCTACGATGAGTGTCCAGAGGTCAATC 600
 QY 201 AlaCysAspGluAsnProAspAlaThrTyrglyArgSerAspIleTrpSerLeuGly 220
 Db 601 GCCTGTGATGAGAACCTGATGCCACTTATGATTACAGAGTATTTTGGTCTTAGGA 660
 QY 221 IleThrAlaIleGluMetAlaGluGlyAlaProProLeuGlnAspMetHisProMetArg 240
 Db 661 ATCAGACCATCGAGATGCGAGAGGAGGAGCCCCCTCTGTGATGATGACCCCATGCGA 720
 QY 241 AlaLeuPheLeuIleProArgAsnProProProArgLeuIleSerIleTyrllePseIleArg 260
 Db 721 GCCCTTCTTCTCATATCTCGGAACCTTCGCGCCAGGCTCAAGTCCAAAGAGTGTCTAAG 780
 QY 261 TyrglyPheIleAspPheIleAspThrCylleValIleTyrglnSerAspArgProProThr 280
 Db 781 AAGTTATTGATCTTCTTATGACATGTCTCATCAAGACTTACTGAGCGGCCACACG 840
 QY 281 GlnGlnLeuLeuIleTyrglnSerPheIleArgAspGlnProThrGluArgGlnValArgIle 300
 Db 841 GAGCAGACTAGAAATTTCCCTTCATCCGAGACCAAGCCCAAGGAGGAGTCCGCAATC 900
 QY 301 GlnLeuIleAspHisIleAspArgSerArgIleValArgGlyGluIleValThrGlu 320
 Db 901 CGCTTAAAGGACCACTTGCATCCGAGAACCGGGGTGAAGAAAGGAGAGACAGAA 960
 QY 321 TyrglyTyrglySerGlySerGluGluIleAspAspSerHisGlyGluGluGluProArg 340
 Db 961 TATGATTAACGCGGACGAGGAGAGATGACAGCCATGAGAGAGAGAGAGAGCCAAAG 1020
 QY 341 SerIleMetAsnValProGlyGluSerThrLeuArgArgGluPheLeuArgLeuGlnGln 360

Db 1021 TCCATCATGAACGTGCTGGAGAGTGCATCTTACGCCCGGAGATTTCTCGGCTCCAGCAG 1080
 QY 361 GlnAsnIleSerAsnSerGlnAlaLeuIleGlnGlnGlnGlnGlnGlnGlnGlnGln 380
 Db 1081 GAAATTAAGAGCAACTCAGAGGCTTTTAAACAGACAGACGACTGTGACAGACAGCAGCAG 1140
 QY 381 ArgAspProGluAlaHisIleTyrglnSerLeuMetHisGlnArgGlnArgIleGluGlu 400
 Db 1141 CGAGACCCCGAGGACACATCAACACCTGTGTGACACAGCGGACCGGCGCATTAAGAGAG 1200
 QY 401 GlnTyrglyGluValArgArgValGluGluGlnGlnGlnGlnGlnGlnGlnGlnGln 420
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 QY 441 GlnArgArgGlnAlaGluArgGluGlnGluTyrlleValArgIleValGluGluGlnArg 460
 Db 1321 GAGCGGCGGACGCGGAGCGGAGAGAGATCAAGCGGAAACAGCTGGAGAGAGCGCG 1380
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 Db 1381 CAGTCAGAACTCTCCAGAGGCGAGCTGACAGAGAGCAATGCTTACTCAAGTCCCTGACG 1440
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 Db 1441 CAGCAGCAACAGAGAGAGAGCTTCAAGAACAGCAGCAGCAGCAGCTCTGCTGGGAGC 1500
 QY 501 ArgIleProLeuTyrlleTyrglyArgGlyMetAsnProAlaAspIleProAlaTrpAla 520
 Db 1501 AGGAAGCCCTTACATTATGTGTGGGCAATGATCCCGTGAACAACCACTGAGGCC 1560
 QY 521 ArgGluValGluGluArgThrArgMetAsnIleGlnGlnGlnGlnGlnGlnGlnGlnGln 540
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 Db 1621 AAGCAGGAGAGAGCGGGGCTAGGCCCTCCATCCCGAGGCTTCCAGAGGCGCCAGGA 1680
 QY 561 ProLeuSerGlnThrProMetGlnArgProValGluProGlnGluIleProHisIle 580
 Db 1681 CCCCTTTCCCAACCTCTCTATGACAGGCGGGTGAAGCCCAAGAGGAGCGGACAG 1740
 QY 580 ----- 580
 Db 1741 AGCTGTGGCACACCGGCTCCACTGAGCCATATGACAGCCTGTACCCCGATCCAG 1800
 QY 581 SerLeuGlnAspGlnProThrArgAsnLeuAlaIlePheProAlaSerHisAspProAsp 600
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 QY 601 ProAlaIleProAlaProThrAlaThrProSerAlaArgIleValAlaIleArgGlnAsn 620
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 QY 641 AspAsnGluAlaProProValProGlnArgThrSerIleAlaThrAlaLeuAsn 660
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 QY 661 ThrSerGlyAlaGlyGlySerArgProAlaGlnAlaValArgAlaArgProArgSerAsn 680
 Db 2041 ACCAGTGGGCGGAGAGGTCCCGGCAAGCCAGGAGAGTCCG----- 2082
 QY 681 SerAlaTrpGlnIleTyrglnGlnArgAlaGluArgGlyThrProIleAspProProGly 700
 Db 2082 ----- 2082

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QY 701 ProProAlaGlnProProGlyProProAlaAlaSerSerAsnProAlaSerLysArgSer 720
Db 2083 -----GCCCCGTAACCCCGGACCTCCAGAGAGAAC 2109
QY 721 AsProGlyTyrTrpGluArgSerAspSerValLeuProAlaSerHisGlyHisLeuProGln 740
Db 2110 GACCTGGCTGGGAAAGCTCGAGACAGCTCTCCAGCTCTCAGCGGACCTCCCGCAG 2169
QY 741 AlaGlySerLeuGluArgAsnArgValGlyAlaSerSerLysLeuAspSerProVal 760
Db 2170 GCTGGCTCACTGGAGCGGAACCGCGTGGAGTCTCTCCAAACCGGACAGCTCCCTGTG 2229
QY 761 LeuSerProGlyAsnLysAlaLysProAspAspHisArgSerArgProGlyLysProAla 780
Db 2230 CTCTCCCTGGGAAATTAAGCCCAAGCCCGACGACCACTCCGCTCACGCGCAGCGCGCGCA 2289
QY 781 AspPheValLeuLeuLysGluArgThrLeuAspGluAlaProArgProProLysLysAla 800
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QY 801 MetAspTyrSerSerSerSerSerGluGluValGlySerSerGluAspAspGluGluGly 820
Db 2350 ATGGACTACTCGTCCGACGAGAGGAGTGAAGAGAGTGAAGACGACGAGAGAGAGGAC 2409
QY 821 GlnGlyGlyProAlaGluGlySerArgAspThrProGlyGlyArgSerAspGlyAspThr 840
Db 2410 GAAGCGCGGCGCAGAGAGGAGAGAGATACCTCGGCGCGCGCAGCATGGAGATACA 2469
QY 841 AspSerValSerThrMetValHisAspValGluGluLysLeuGlyThrGlnProPro 860
Db 2470 GACAGGCTACGACCATGATGCTCCAGCGTGCAGAGATCACCGGAGCCAGAGCCCA 2529
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QY 941 GlnProGlyGlySerGlyAspSerLysProLysLeuValGlyGlyGluGlyThr 960
Db 2770 CAGCCTGGAGGAGTGGGAGCAGATCCCATCACAGCTTGTGATGTGAAGAGGCACT 2829
QY 961 ArgLeuAspGlnLeuGlnTyrAspValArgLysGlySerValValAsnAlaAsnProThr 980
Db 2830 CGGCTGACAGCTGAGTACGACGAGAGAGGTTCTGTGATCAACCTGAATCCAC 2889
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Db 2950 GAGATCTCTGTGCGAGCCCTTGGGGGGTCAACTGCTGTGGTGGGCGAGAGAACGGGCTG 3009
QY 1021 MetLeuLeuAspArgSerGlyGlnGlyLysValTyrGlyLeuLysGlyArgArgPhe 1040
Db 3010 ATGTGTGCGACCGAAGTGGCGAGGCAAGGTATGAGCTATTGGGGGCGAGGCTTC 3069
QY 1041 GlnGlnMetAspValLeuGluGlyLeuAsnLeuLeuLysLeuHisSerGlyLysArgAsn 1060
Db 3070 CAGCAGATGAGTGTGTGAGGGGGCTCAACTGCTCATCAACATCTCAGAGAGAAAGAAC 3129

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QY 1061 LysLeuArgValTyrTyrLeuSerTrpLeuArgAsnLysLeuHisAsnAspProGlu 1080
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QY 1081 ValGluLysGlnGlyTyrThrThrValGlyAspMetGluGlyCysGlyHisTyrArg 1100
Db 3190 GTGAGAAAGAGCAGAGGCTGAGCACCTGGGGGAGATGAGAGGCTCGGGGACATACCGT 3249
QY 1101 ValValLysTyrGluArgGlyLysPheLeuValHisAlaLeuLysSerSerValGluVal 1120
Db 3250 GTTGGAAATACGACCGGATTAAGTTCTGTGATCGGCTTCMAAGCTCCGTGAGGAG 3309
QY 1121 TyrAlaTTrpAlaProLysProTyrHisLysPheMetAlaPheLysSerPheAlaAspLeu 1140
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QY 1141 ProHisArgProLeuLeuValAspLeuThrValGluGluGlyGlnArgLysValHis 1160
Db 3370 CCCCACCGCCCTCTGCTGTGACCTGACAGTGAAGAGAGGAGGACGCGCTCAAGGTCATC 3429
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 ORGANISM Homo sapiens
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 REFERENCE Dan, I., Watanabe, N. M., Kobayashi, T., Yamaehita-Suzuki, K., Fukagawa, Y., Kajikawa, E., Kimura, W. K., Nakashima, T. M., Matsumoto, K., Niimiya-Tsuji, J., and Kusumi, A.
 Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development

JOURNAL EEBB Lett. 469 (1), 19-23 (2000)
 MEDLINE 20175403
 PUBMED 10708748
 REFERENCE 2. (bases 1 to 3888)
 AUTHORS Dan, I., Matanabe, N.M. and Kusumi, A.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1999) Ippetta Dan, EPATO, Kusumi Membrane
 Organizer Project: 5-11-33 Chiyoda, Naka-Ku, Nagoya, Aichi
 460-0012, Japan (E-mail: dangb@ic.nagoya-u.ac.jp,
 Tel:81-52-789-2497, Fax:81-52-789-2968)
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Oy	270	LeuIleLys-----ThrTyr-----LeuSerArgPro	278
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Oy	279	ProThr-----GluGlnLeuLeuLysPheProPheIleArgAspGlnProThr	294
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US-10-029-115-2 (1-1312) x ab035698 (1-3888)

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DB 2995 ACGGAGAAAGGAGCTGATGTCTGACCAAGTGGGAGAGGAGAGTGTATGACTCAT 3054
QY 1036 GlyArgArgArgPheGlnGlnMetAapValLeuGluGlyLysAsnLeuLeuLysThrLys 1055
DB 3055 GGGGCGGCGAGCGCTTCAGAGATGATGTGTGAGAGGGGCTCAACTGTCTATCAACATC 3114

```

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QY 1056 SerGlyLysArgAsnLysLeuArgValTyrTyrLeuSerTrpLeuArgAsnLysLysLeu 1075
DB 3115 TCAGGGAAAGAAACAACATGGGGGTATTAATCTGTCTGTGCTCCGAAACAAGATTCG 3174
QY 1076 HisAapAapProGluValGluLysLysGlnGlyTTPThrThrValGlyAapMetGluGly 1095
DB 3175 CACAATGACCCAGAGATGGAGAAAGAGAGGCTGAGACACCGTGGGGAGCATGGAGGAG 3234
QY 1096 CysGlyHisTyrArgValValLysTyrGluArgLysPheLeuValLysLysLeuLys 1115
DB 3235 TGGGGGCACTACCGTGTGTGAATAACAGCGGATTAAGTTCTCTGTCTATCCCTCAAG 3294
QY 1116 SerSerValGluValTyrAlaTrpAlaProLysProTyrHisLysPheMetAlaPheLys 1135
DB 3295 AGCTCCGTGAGGTATATGCTGGGCGCCCAACCTTACCAATTCATGGCTTCAAG 3354
QY 1136 SerPheAlaAapLeuProHisArgProLeuLeuValAapLeuThrValGluGluGln 1155
DB 3355 TCCTTTCGCACTCCCGCACCGGCGCTGTGCTGAGCTGACATGACATGAGAGAGGAGGAG 3414
QY 1156 ArgLeuLysValLysTyrGlySerSerArgLysPheHisAlaValAapValAapSerGly 1175
DB 3415 CGGCTCAAGGTCACTATGATGCTCCAGTGTGCTGCTTCACTGTGTGATGTGCACTCGGAG 3474
QY 1176 AapSerTyrAapLysTyrLysProValHisLysGlnSerGlnLysThrProHisAlaLys 1195
DB 3475 AACAGCTATGACATTTACATCTCTGTGACATCCAGACCGAGATCAAGCCCATTCATC 3534
QY 1196 IlePheLeuProAsnThrAapGlyMetGluMetLeuLeuCysTyrGluAapGluVal 1215
DB 3535 ATCTTCTCCCGCAACACCGAGCGGATGAGATGCTGCTGTGCTACAGAGAGAGGAGTGC 3594
QY 1216 TyrValAsnThrTyrGlyArgLysLysLysAapValValLeuGlnTTPGlyGluMetPro 1235
DB 3595 TACGTCAACAGTACGGGCGCATTAAGATGTGTGTGTGCTGACAGTGGGGAGATGTCT 3654
QY 1236 ThrSerValAlaTyrLysCysSerAsnGlnLysMetGlyTTPGlyGluLysAlaLysGlu 1255
DB 3655 ACTTGTGTGCTTACATCTGTCTCCAAACAGATATGGCTGGGGTGAAGAACCTTGAAG 3714
QY 1256 IleArgSerValGluThrGlyHisLeuAapGlyValPheMetHisLysArgLysLysArg 1275
DB 3715 ATCCGCTGTGTGAGAACGGGCGACCTGACGGGCTTCAAGCAAAACAGCTCAGAGG 3774
QY 1276 LeuLysPheLeuCysGluArgAsnAapLysValPhePheAlaSerValArgSerGly 1295
DB 3775 CTCAAGTTCTGTGTGAGACCGAATGACAAGGTGTTTGTGCTCAGTCCGCTCTGGGGGC 3834
QY 1296 SerSerGlnValTyrPheMetThrLeuAsnArgAsnCysLysMetAsnTrp 1312
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RESULT 2
 AB035698.C
 TOIG of: ab035698 check: 9874 from: 1 to: 3888

LOCUS AB035698 3888 bp mRNA linear PRI 16-APR-2000
 DEFINITION Homo sapiens mRNA for Mischapen/NIK-related kinase MINK-1, complete
 cde.
 ACCESSION AB035698
 VERSION AB035698.1 GI:6970477
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
 Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
 Matsumoto,K., Niimoriya-Tsujii,J., and Kusumi,A.
 Molecular cloning of MINK, a novel member of mammalian GCK family
 kinases, which is up-regulated during postnatal mouse cerebral
 development

QY	326	erglgluglgluabpa	serthi	sgl	ylgluglglu	glu	pro	ser	ser	ile	met	an	val	346
Db	3018	--CAGCA	-----CAT	-----	CAAGCC	-----	GTTCCTC	-----	GTTCCTC	-----	GTTCCTC	-----	GTTCCTC	
QY	346	ro	gl	gl	gl	gl	gl	gl	gl	gl	gl	gl	356	
Db	2992	CCACGACGAGTTGAC	CCCCCCCCAGGGCTGCACAGAGATCTCGAGTTGAA	TTGGCTTCT	2933									
QY	356	eu	-----Arg	-----	leugl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	371	
Db	2932	TGTACTTCCGAGTTC	-----AGG	-----	GATC	-----	GATC	-----	GATC	-----	GATC	-----	GATC	
QY	371	ngl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	390	
Db	2893	-TG	-----TTGG	-----	TGGGATTCAGCTTGAC	-----CAC	-----	AGAACCC	2862					
QY	390	eu	leu	hi	sgl	arg	gl	arg	arg	ile	gl	ugl	ngl	408
Db	2861	TTCTTCA	-----CGTGTACTG	-----	CAGC	-----	TGTGTAGCCAGAT	2827						
QY	408	lgl	ugl	gl	gl	gl	gl	gl	gl	gl	gl	gl	420	
Db	2826	GCCCTCTCACCCACTAGAGCGCTGATGGAGATGCTGTCCCACTGCTCCAGGCTGTA	2767											
QY	420	ys	-----leugl	gl	ly	ys	gl	ngl	ngl	arg	-----Arg	leugl	ab	436
Db	2766	GATCCCTAGATCCACAA	-----CATGCTGACAGAGCTC	-----TTGCCAGGGGCTT	2719									
QY	437	---Arg	-----Arg	gl	ugl	arg	gl	al	sgl	arg	gl	ngl	ngl	453
Db	2718	TACCAAGCCACAGAC	-----TGAT	-----AGTACACATCCCAATCC	TTCCAGAGGTGG	2671								
QY	454	lys	gl	ngl	ugl	gl	ngl	arg	gl	ngl	ser	gl	ngl	473
Db	2670	G	-----CTT	-----TGCGCT	-----TTG	-----CTG	-----	CTG	-----	CTG	-----	CTG	2655	
QY	474	Ala	ly	-----	leu	lys	ser	leugl	ngl	ngl	ngl	gl	ngl	487
Db	2654	---TTCTCGAGTGGAGTGGCTGGG	-----CTG	-----GACACGTGACAGGT	2612									
QY	488	leu	-----glu	lys	gl	ngl	ngl	ngl	ngl	ngl	ngl	ngl	505	
Db	2611	TTGTGTACCA	-----TTGCTGTACGATGACAGCGG	-----T	2579									
QY	505	yr	hi	-----tyr	gl	ys	arg	gl	yl	-----Met	Asn	Pro	Ala	522
Db	2578	TCCGCTCTCTTC	-----AGGGGTGCGCTGGA	CCA	-----CCA	-----TGGTG	CCGC	2537						
QY	522	lu	val	gl	ugl	arg	th	arg	-----Met	Asn	lys	gl	ngl	539
Db	2536	-----CCCCGTA	-----TGGGGGCTGGGTCCCGGT	-----GAT	-----CTCTTCGAGCT	2498								
QY	540	Ser	ly	Pro	gl	ys	ser	th	gl	yl	Pro	gl	Pro	558
				</										

Db	2342	TTGGG--AGGCCGAG-----GGGCTTCGT--CCAGATCCGCT-----CTT	2306
Qy	656	AlaThr-----AlaLeuAsnThrSerGlyValaGly--GlySerArgProAlaGlnAlaVal	673
Db	2305	TCAGAACACAAAGACTCTGC-----GGGCG-GGCCCTGGC--CGT-----GAG-----	2268
Qy	673	AlArg-AlaArgProArgSerAsnSerAlaTrpGlnIleTyrLeuGlnArg--ArgAlaG	692
Db	2267	--CGGTGGTTCGT--CCG-----GCTTTGG--CTTTATT--CCAGGGGAGAG--C	2229
Qy	682	IuArgGlyThr--Pro-----Lys--ProPro-Gly-Pro--ProAlaGlnPro-P	706
Db	2228	ACAGGGAGCGTCCGCTTTGGAGAGACTCCACAGCGGTCCCTCAGT-GAGCCAGC	2170
Qy	706	roGlyProProAsnAlaSerSerAsnProAlaLeu--Arg-ArgSerAspProGlyTrpG	725
Db	2169	CTGGGG-----GAGTGGCCCGTGAGA-----GGCTGG-2143	
Qy	725	IuArgSerAspSerValleu-ProAla--SerHis--GlyHisLeu--Pro-GlnAlaG	742
Db	2142	--AAG--GAGC-----CTGTCCAGCGTTCCACAGCAGGGTCAGCTCTCCTGAGGTGG	2093
Qy	742	IySerLeuGlnuArgAsnArg-----ValGlyAlaSerSerLys--LeuAspSerArg	759
Db	2092	GG--TTAC--TGCA-CGAGCTCCGTGGT-----GGCCGGAGACCTCC-G-GCC	2048
Qy	759	ro--Valleu--SerProGlyAsnLysAlaLys-Pro--AspAlaHis--ArgSerArg	775
Db	2047	CACGTGTATTAGGGCAGTGGCAGTATAGC-AGTCTCTTGAGG-CACCTGGG--TGG	1993
Qy	776	ProGly--ArgProAlaAspHeValleuLeuLys-GluArgThrLeuAspGlnAlaPro	794
Db	1992	--GGCTCGT-----TAT--CTGGG-CGAGCCAGG--CTGGGGGATTCCGGG	1952
Qy	795	Arg--Pro--Pro-LysLys-AlaMet-AspTyrSerSerSerSerGlnu-----Va	810
Db	1951	TGGGGCCAGGTCTTCAGAGGTGGGTGTGAATCTG-GCG-----GATGACAGCTCT	1899
Qy	810	IGluserSerGluAspAspGlnuGlnuGlnu-Gly-GlyProAlaGlnuLys	829
Db	1898	C-----GGCACGTGGGCTGGC-----AGTGGTG-C	1873
Qy	829	rg-AspThrProGly--GlyArgSerAspGlyAspThrAspSerValSerThrMetVal	848
Db	1872	GGGGAT-----GGCAGGGTCGG-----GGT-----	1853
Qy	848	AlHisAspValGlnGlnIleThrGlyThrGlnProProTyrGlyGlyThrMetVal	866
Db	1852	--CATG-G-GAGG-CTG--GGAAGCAGCAGCAGGTTTCG-GGTGGG--CTGTCTC	1809
Qy	868	AlGlnArgThrProGlnuGlnu--GluArg--AsnLeuLeuHisAlaAspSerAsnGly	885
Db	1808	TGC--AGG-----GACTGGGATGGGGTACAGGTGCGCATAT-----GGC	1770
Qy	886	TyrThr--Asn-----LeuPro-Asp--ValValGln-----ProSer--His	899
Db	1769	TTCAGTGGAGACCGGTGTGCACACAGGCTGTGGGGCTCCCTCGGGGTCCACCGGC	1710
Qy	899	ro-----Thr-GluAsnSerLysGlyGlnSerPro-----Pro-SerLys-----	911
Db	1709	CTTCGATACAGAGAGAGTCTGGGAAAGGGGT-----CTGGGGGGCCCTGGAGAGCCTGGG	1654
Qy	912	AspGlySerGlyAspTyrGlnSerArg-----GlyLeuValLysAlaPro-GlyLys	929
Db	1653	GATGGG--GGG--CTCAGGCCCGCGTGGCTCGGTCTCTCTT-CG-CGAGGGAGAG	1602
Qy	929	erSerPhe-Thr-MetPheValAspLeu--GlyIle-Tyr-----Gln-C-ProGly-Gl	944
Db	1601	-----TTCTGTGCTGTTCATCC--TTGTTCCTCTTACCTGCGGGCCAGGCTGG	1549
Qy	944	Y--SerGlyAspSerIle-----Pro-Ile--Thr-AlaLeu-ValGlyGl	957

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Db      1548 TTGTCAGCGGG-----ATTCAATGCCCGACCATATAGTACAGGGCTTCCTGTCGCC 1495
QY      957 YGIUGLYThrArg-----Leu--AspGlnLeuGlnTyr--Asp----- 968
Db      1494 A---GGC---AGGAGCTGCTGCTGCTG---CTGT--TTCTGAAGCTCTGCTGCTGCT 1445
QY      969 ---Val-Arg-----Lys--Gly--Ser-ValValAsnValAsnProThrAsnThrAr 983
Db      1444 GGTGTCGACGAGGACTGAGTAGGATGATGCTCTGCTGACAGCTG---CTCC--T--GG-AG 1393
QY      983 GAlaHisSerGlu-----ThrPro-GluIle---ArgLys-Tyr----- 994
Db      1392 A---GGTTCGTGACTGCTGCTGCTCTCCAGCTGCTTCCTG---GTAATTCCTGCTGCGCT 1337
QY      995 -Lys-----LysArg-----Phe-Asn-SerGlu-Ile-----Leu-----CysA 1005
Db      1336 CCGCTGCGCGCGCTCTCTCTCCCGCGAGACCTGCAATGCTCTCAGCCGCGCTGCT 1277
QY      1005 LAAlaLeu-TyrGlyValAsnLeu---LeuValGlyThrGluAsnGlyLeuMetLeuLeu 1023
Db      1276 --G---CTCCTTCCTC-CTGCAGCTTCGGCTGCTCCGCC--TCCCG-CCGCTGTGCTCTC 1225
QY      1024 AsparGserGlyGlnGly--Lys-Val-TyrglyLeuIle---Gly-Arg---Arg--- 1038
Db      1224 CA-CGC-----GGCCCGCTCTCTCTCTCTG-CTCCTCTATGCGCGCTGCCCTG 1176
QY      1039 ---Arg--PheGln-----Gln--MetAsp-----ValLeuGluGlyLeuA 1050
Db      1175 TGCAGCAGGTGTATGATGTGTGCTCGGGCTCTGCTGCTGCTGCTGCTGCAAG--CTG- 1120
QY      1050 snLeuLeuIleThrIleSerGlyLysArgAsnLysLeuArgVal-Tyr-Tyrlensert 1069
Db      1119 --CTGCTGCTGCTT-TTA-----AAGCC-TCGTAGTTG---CTCTATATTTCCTGC--TG 1075
QY      1069 P-----Leu-ArgAsnLysIle--LeuHisAsnAspProGluValGluLys-Ly 1084
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QY      1084 sGlnGly---TyrThrThrVal-GlyAsp-MetGluGlyCysGlyHis-TyrlargValA 1102
Db      1027 TGAATGAGCTTG---CTCTCTCTCTCTCTCAATGAGCTGT---CATCTTC---CTCCT 980
QY      1102 L-----Lys--TyrgluArgIleLysPhe-Leu-Val--IleAlaLeuLysSerSerVal 1118
Db      979 CGCTGCGCTGACTCA-----TATCTGTCTCCTCTT--CTC--ACCCCG--- 937
QY      1119 GluVal-Tyr-----AlaTyr---AlaPro-----Lys 1126
Db      936 ---CTTCTTCGGGATCGGTCAATGTGTCTTAACTGATCGGACCTGCCGCTCCGT 880
QY      1127 ---Pro-----Tyr----- 1128
Db      879 GGGCTGCTCCCGATGAAAGGAACTTCACTGACTGCTCCGCTGCGCGGCTCAGTA 820
QY      1129 ---His-----Lys-----PheMetAla--Phe----- 1134
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QY      1135 ---Lys-SerPhe-----AlaAsp--Leu-----ProHi 1142
Db      759 GAGCTGCGGGGAGGCTCCGAGAAATGAGAGAGGCGCTCGCATGGGCTGATGCACA 700
QY      1142 sArg-----ProLeu---LeuValAspLeuThrValGluGluGly---GlnArgLeu--- 1157
Db      699 CAGAGGGGGGCTCCCTCTGC-CATCTC-----GATGGCTGTGATTC-CTAGAGA 652
QY      1158 --LysValIleTyr-----GlySerSerAlaGlyPhe---His----- 1168
Db      651 CCAAA-----TATCACTCTCTTAATCATATAGTG--GCATCAGGCTTTCATACACAGCG 600
QY      1169 ---AlaValAsp--ValAspSerGlyAsn-SerTyrAsp-IleTyr---IlePro--- 1183
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QY      1184 ---ValHisIleGlnSerGlnIleThrPro-----His-AlaIle-Ile-----Phe-- 1197
Db      541 TGGGTTCCAGCTG---AGCA--CTCACCACCAAAATCACTAGCTGACTGCACTTCTTC 487
QY      1198 ---LeuPro--Asn---Thr--Asp-----GlyMetGluMet 1206
Db      486 TGTCAAGACACATTCCTGCTGATGTCTCGATGATCACTTGTGGCATGGAGATG 427
QY      1207 ---Leu-----Leu--Cys---TyrgluAspGluGlyValTyr-ValAsnThr 1219
Db      426 GGCCAGACCCCTGAGGATCTCCCTCAGATATA-----GGCA-TACAGTCC--TCC 378
QY      1220 Tyr-GlyArg---IleIle-----LysAspVal-Val-----L 1229
Db      377 TTCAGGGGCTTCCCTTTGTGTCTTTACAGGTGATGATCACTGAACACAGACACAGAC 318
QY      1229 euGln-----TyrglyLysMetProThrSerValAlaTyrIle----- 1241
Db      317 TCCATCACACAGCAGAGCTGATCATGCTTCCCGGGGGCTC---TTCCTGATGAAGCT 261
QY      1242 ---CysSerAsnGlnIleMetGlyTyrglyGluLysAlaIleGluI 1256
Db      260 CCGTAGTAGTGGCGATGT--G--CGG-----TGGT--G--AGA--GTA--CT 224
QY      1256 e---ArgSerValGluThrGlyHisLeu-----AspGlyValPheMetHisLys-----A 1272
Db      223 TTTTACAGATGTAT-----CTCCTGTGTAT--CTCTCTCTCT--CTGCTCTCC 177
QY      1272 rGAla-----Gln--Arg-----Leu--LysPheLeu---CysGluArgAsnA 1284
Db      176 GTGACATCATGACCTTGATGGCAGCAGCTGCCCTGTC--TTGACATGC--CGACC- 123
QY      1284 sPlyValPhePheHisSerValArgSerGlyGlySerSerGluValTyr-Phe----- 1301
Db      122 ---TTGTACA--CCTGTCCG1-----AGC---TTCATTGCCGAC 91
QY      1302 ---Met-Thr--Leu--Asn-----Arg---Asn-----Cys-Ile 1309
Db      90 CACCTTCACAACTCAAAAGATCCAGCAGAGGCTCCGACAGGGCGGACAGGTGATGCTGC 31
QY      1310 ---Met-----AsnTyr 1312
Db      30 CAGCTGCGGGCGGGGCTG 10

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Search completed: April 19, 2005, 10:13:39
 Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 19, 2005, 10:19:23, Search time 8 Seconds

(without alignments)
1.275 Million cell updates/sec

Title: US-10-029-115-2

Perfect score: 13011
Sequence: 1 MGDPAFSLDIDLSALRD.....SGSSQVYFMTLNRCINMW 1312

Scoring table: BLOSUM100

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Searched: 1 segs, 3888 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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Database: ab035698.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6318.66	48.6	3888	1	ab035698 TOIG of: ab035698

ALIGNMENTS

RESULT 1
ab035698

TOIG of: ab035698 check: 9874 from: 1 to: 3888

LOCUS AB035698 3888 bp mRNA linear PRI 18-APR-2000
DEFINITION Homo sapiens mRNA for Mischapen/NIK-related kinase MINK-1, complete cds.

ACCESSION AB035698
VERSION AB035698.1 GI:6970477

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1 (sites)
Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.

AUTHORS

Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita, Suzuki, K.,
Pukagaya, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M.,
Matsumoto, K., Nimomiya-Tsuji, J., and Kusumi, A.
Molecular cloning of MINK, a novel member of mammalian GCK family
kinases, which is up-regulated during postnatal mouse cerebral
development

JOURNAL

FEBS Lett. 469 (1), 19-23 (2000)

MEDLINE

20175403
10708748
2 (bases 1 to 3888)

REFERENCE

Dan, I., Watanabe, N.M., and Kusumi, A.
Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
Direct Submission
Organizer Project: 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
460-0012, Japan (E-mail: dangobio.nagoya-u.ac.jp,
Tel: 81-52-789-2497, Fax: 81-52-789-2968)

JOURNAL

FEATURES

source

gene

CDS

1. 3888
/gene="MINK"
/note="Human MINK is a conceptually translated protein
using mouse MINK sequence and the human genomic clone
hRPK17.H.5 from chromosome 17. Human and mouse MINK
shares 97% amino acid sequence identity and all 32
exon/intron boundaries in CDS matched consensus sequences
for splicing."
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/protein_id="BAA90753.1"
/db_xref="GI:6970478"

ORIGIN

AB035698

Length: 3888

April 15, 2005 16:45

Type: N

Check: 9874

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Pred. No.:

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Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

1

2

101

1

3888

1273

92.65%

92.65%

96.91%

1

1

1

1

1

1

1

1

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1

1

1

1

1

1

1

US-10-029-115-2 (1-1312) x ab035698 (1-3888)

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 QY 21 ProAlaGlyIlePheGluLeuValGluValAlaGlyAsnGlyThrTyrglyGlnValTyrg 40
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 QY 41 TyrglyArgHisValIleTyrglyGlnLeuAlaAlaIleTyrglyValMetAspValThrGlu 60
 Db 121 AAGGGGCGGCATGTCAAGACGGGGGAGCTGGCTGCATCAAGGTCATGATGTCAAGAG 180
 QY 61 AspGluGluGluGluIleTyrglyGlnIleAsnMetLeuIleTyrglySerHisAspArg 80
 Db 181 GACGAGGAGGAGAGAGATCAAAACGAGGATCAACATCTGAAAAAGTACTTCCACCCAGCCG 240
 QY 81 AsnIleAlaThrTyrglyTyrglyAlaPheIleTyrglySerProProGlyAsnAspAspGln 100
 Db 241 AACATGCGCACTTACTTACGAGAGCTTCTCATCAAGAAAGACCCCGGGGAAACATGACAG 300
 QY 101 LeuTrpLeuValMetGluPheCysGlyAlaGlySerValThrAspLeuValIleAsnThr 120
 Db 301 CTCTGGCTGGTATGAGATTCTGTGGTCTGTGCTTCACTGACTGACCTGGTAAAGACACA 360
 QY 121 TyrglyAsnAlaLeuIleTyrglyAspCysIleAlaTyrglyIleCysArgGluIleLeuArgly 140
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 QY 141 LeuAlaHisIleuHisAlaHisIleValIleHisArgAspIleTyrglyGlnAsnValLeu 160
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 QY 221 IleThrAlaIleGluMetAlaGluGlyAlaProProLeuCysAspMetHisProMetArg 240
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 QY 241 AlaLeuPheLeuIleProArgAsnProProProArgLeuIleSerTyrglyTrpSerTyrg 260
 Db 721 GCCCTCTTCTCATCTCTGGGAACTCTCGGCCAGGCTCAAGTCCAAAGAGTGTAAAG 780
 QY 261 TyrglyPheIleAspPheIleAspThrCysLeuIleTyrglyLeuSerArgProProThr 280
 Db 781 AAGTTCATGATCTTCACTTACACATGTCTCATCAAGACTTACCTGAGCCGCCACCAAG 840
 QY 281 GluGlnLeuLeuIleTyrglyPheProPheIleArgAspGlnProThrGluArgIleValArgIle 300
 Db 841 GAGCAGACTAGTGAATTTCCCTTCATCCGGGACCAAGCCCAAGAGCGGAGCTCCGATC 900
 QY 301 GlnLeuIleAspHisIleAspArgSerArgIleTyrglyValArgGlyIleValThrGlu 320
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 / REFERENCE 1 (bases)
 / Dan,i., Macanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
 / Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
 / Matsumoto,K., Niimoriya-Tsuji,J. and Kusumi,A.
 / Molecular cloning of MINK, a novel member of mammalian GCK family
 / kinases, which is up-regulated during postnatal mouse cerebral
 / development

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JOURNAL      FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE      20175403
PUBMED       10708748
REFERENCE    2 (bases 1 to 3888)
AUTHORS      Dan, I., Matanabe, N.M. and Kusumi, A.
TITLE        Direct Submersion
JOURNAL      Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
              Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
              460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp,
              Tel: 81-52-789-2497, Fax: 81-52-789-2568)
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AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.

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 Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita, S., Suzuki, K., Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Niimura, T., and Kusunoki, A.
 Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development
 JOURNAL FEBS Lett. 469 (1), 19-23 (2000)
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 PUBMED 10708748
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 Dan, I., Watanabe, N.M., and Kusunoki, A.
 Direct Submision
 JOURNAL Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusunoki Membrane Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dan@bio.nagoya-u.ac.jp, Tel: 81-52-789-2497, Fax: 81-52-789-2968)

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OY 3722 ---CCT---A-----CATC-TGCTC-----CAACA-GA---TAATGGGCTGGG 3754
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AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.

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QY	1567	CGAAGGTAGAAAGAGAACAAAGATGAAACAGCAGCAGAACTCTCCCTTGGCCAAAGC	1626
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 REFERENCE 1 (Siles)
 Dan, I., Matanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Nimomiya-Tsuji, J. and Kusumi, A.
 Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development
 JOURNAL FEBS Lett. 469 (1), 19-23 (2000)
 MEDLINE 20175403
 PUBMED 10708748
 REPERENCE 2 (bases 1 to 3888)
 Dan, I., Matanabe, N.M. and Kusumi, A.
 Direct Substitution
 JOURNAL Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel: 81-52-789-2497, Fax: 81-52-789-2966)
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QY	1447	CAGCAGCAACAGCAGCAGCAGAGCTTTCAAGAAACAGCAGCAGCAGCAGCTTCGGCTGGGAGC	1506
Db	1441	CAGCAGCAACAGCAGCAGCAGCAGAGCTTTCAAGAAACAGCAGCAGCAGCAGCTTCGGCTGGGAGC	1500
QY	1507	AGGAAGCCCTCTGTACATTATATGTCTGGGGCATGAAATCCCGCTGACAAACCAAGCTTGGGCGC	1566
Db	1501	AGGAAGCCCTCTGTACATTATATGTCTGGGGCATGAAATCCCGCTGACAAACCAAGCTTGGGCGC	1560
QY	1567	CGAGAGGTAGAAAGAGAGAACAAAGGATGAAACAGAGCAGAGAACTTCCCTTGGCCAAAGAGC	1626
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VERSION AB035698.1 GI:6970477
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ORGANISM Homo sapiens
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REFERENCE
1 (bases)
AUTHORS Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,
Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,
Matsumoto,K., Niimiya-Tsuji,J. and Kusumi,A.
TITLE Molecular cloning of MINK, a novel member of mammalian GCK family
kinases, which is up-regulated during postnatal mouse cerebral
development
JOURNAL FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE 20175403
PUBMED 10708748
REFERENCE
2 (bases 1 to 3888)
AUTHORS Dan,I., Watanabe,N.M. and Kusumi,A.
TITLE Direct Sublabation
JOURNAL Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
460-0012, Japan (E-mail: dan@bio.nagoya-u.ac.jp,
Tel:81-52-789-2497, Fax:81-52-789-2968)
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Search completed: April 19, 2005, 09:57:37
Job time : 25 secs

; AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.

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 / REFERENCE 1 (ites)
 / AUTHORS Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita, Suzuki, K., Fukagawa, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Niimiya-Tsuji, J. and Kusumi, A.
 / TITLE Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development
 / JOURNAL FEBS Lett. 469 (1), 19-23 (2000)
 / MEDLINE 20175403
 / PUBMED 10708748
 / REFERENCE 2 (baee 1 to 3888)
 / AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.
 / DIRECT SUBMISSION Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dan@bio.nagoya-u.ac.jp, Tel: 81-52-789-2497, Fax: 81-52-789-2966)
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ab035698
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DB 3826 ---AGC--GACCTGAGGCAAAAAC-ACCTTGCTATTCGCTC-----ACAC--AG 3784
QY 75 GATCTT-----TGAGCTTGAGAGGTGGTGGCAATG--GAACCTAGC--GACAGGT 123
DB 3783 GAACTTGAGCCTTGAGCTGCTT-----TTGT--GC-ATGAAGACC--CCTCG--AGGT 3736
QY 124 -----T--ACA-AGAGTCGAGCATGTCAAGACGGGCAAGCTGCT-----GCC 162
DB 3735 GCCCGTCTCCACAGAG--CGG-ATCTCA-----TGGCTTTTCACCCAGCC 3691
QY 163 ----ATCAAGGTATG-----GATGTACGAGAG--ACGAGAGAGAGATCAAAAG 211
DB 3690 CATTATC-TGGT--TGAGCAGATGT-----AGGCCA--A-GAAG--T-----AG 3652
QY 212 AGATCAACATGCTGAAGAAAGTATCTACACACCGCA-----ACAT-----CGCC 255
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QY 256 ACCTAC-----T-ACGAG--CCT--TCATC--AAG-A-AG-AGC-----CC--C- 290

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QY 325 TTCTGT-G--GT-----GCTGGTTC--AGT-GACTGACCTGTAAAGACAAAGGC 372
DB 3493 ---TGATGATGATCATGCT-GTTCGCCAGGTGAC--ATC-----CACA-----GC 3454
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DB 3414 -CT-GCCC--CTCCTTACTGTTC--AGTGA--CCAGC--AGA-----GGGC-G-- 3376
QY 481 GTGCTGCTGACAGAGATGCTAGGTC--AAG--CT--AGTG--GATTTGGGGT 527
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DB 2986 GC--AGS-----TTGACC--CCCCAAA-----GGGCTG-CACGAGAGATCTG--G 2948
QY 965 AATATGA-----GTA--CAGCGG--CAGCGAG--A-----GGAATGAC 999
DB 2947 AGT-TGAATCGCTTCTTGTACTTC--CGATCTCAG-G-GGTCTCACTGTG----- 2901
QY 1000 AGCC-----ATGAGAGAGAAAG-----GAGCA-AG--C-TGCATCA--T-GA 1036
DB 2900 -GCCCGGAGTGTGGT--GATTCACGTTGA-CCAAGAACCTTTC-TCAAGTCT 2849
QY 1037 AGCTGC--CTGAGAGTCACTTACGCGGAGATTCTCCGGCTCCAGAGAAATTA 1094
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 Db 2657 CTGTTCTCG-GTG--GGTG--AGTGGCTGG--GCTGAGCA-CTGACG--GGAAGTTTG 2609
 Qy 1274 -----AG-AAGAGCAG-----CAGCGCG-GCTGAGGA 1301
 Db 2608 TGTATCCATTGCTGTGATGATGACATGACAGGTTCCGCTCTCTTCAGGGGTGCGCTGAGCA 2549
 Qy 1302 CATGCA-GGCTGCGGGC-----GGGAGAGAGCGGGCGGAGG---CGAGGGTGA 1349
 Db 2548 C--CATGG--TGGCGCCCCCTATGGG-----GGCTG--GGTCCG---GTGA 2510
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 Db 2509 TC-----TCTGAC--GTGG-----TGACACACATGATGCTGAC-GCTGTCTGA 2466
 Qy 1396 CGTCTCAAGAGCA--GCTGACG---CAGAGCATGCTAC--CTCAATCTCTGACG 1447
 Db 2465 --TC-CC-----CATGCTGCGGCCCCAGGGGTAT--CT-CTGCTC--CCCT----C 2425
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 Db 2424 TGGTG---GC--CCGC--CTTC-----GC--CTTCTCTCTGCTGCTCA-CTGG 2384
 Qy 1493 T-----CTGCTCTGG--GGAC--AGGAAGCCCTGTA--CCATTATG--TC----- 1531
 Db 2383 TTTTCACTT-CCTCGCTGACACGA-----GTAGTCC--ATGGCCTCTTGGGAAG 2335
 Qy 1532 ---GGGCGAT-----GAATCCGCT-----G--ACAA-----CCAGCTTG 1562
 Db 2334 CCGAGGGGCTGCTGCAGAGT--CCGCTTTTTCAGCAACAAAGTCTGCGGCGGCTG 2276
 Qy 1563 GGGCCGAGAG-----GT-----AGAGAGAAACAAAGATGA 1595
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 Qy 1596 CAGC-----AGCAGACTC-----TCC-CTTGAGCA--AGACAGCA 1632
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 Db 2087 CTGGCAGGAC-----TGCTG-----GGCTG----- 2066
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 Db 2065 -CCC-----G--GACCCCT-----CGGGC-CCCACTG-----GT---GTTA 2037
 Qy 1845 AGGAGC--TGTG-ATCCGCAAGATTCAACCCCACTCTGAAG--ACCT-----GGCC 1894
 Db 2036 AGG-AGAGTGGCAT-----AGA--TGAG--GTCTCTG--AGGACCTTGGGTGG-- 1992
 Qy 1895 CCAGCC-CG-AATC-----C--CCAGCCTGGGTCCGCCAGATTAAGAGC-----CCC 1940
 Db 1991 ---GCTTCTTATCTGGGAGGAGCCAGGCTGG---G-----GAT-TCG-GGCTGGGGCC- 1945

Qy 1941 ACCAAGGNGCC-TGAGA-----GSACTCA---TCT-----ATGGCACTGC-CCTTAAC- 1986
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 Qy 2062 TA-----T-CTGA-AAGG---CGGCAAGCGGGGACCCCAAG-----CCTCAAGGC 2107
 Db 1788 TACAGGTCTGATATAGCTT-----AGTGG--ACCC-----GATGTCACCAAGG-- 1743
 Qy 2108 CCCC---TGC--TCAGCCCTTGGCCCGCCCAACGCTTATGAACCCGACCTC----- 2157
 Db 1742 -CTTTGTGCGGT--CTTCTGG-----GGCTC-----CAGCGGCTTGGCAT 1702
 Qy 2158 AGAGAGCGACCTTGGCTGGAGCGTTCGACAGCTCT---TCG---A-GCTT 2206
 Db 1701 AGAGAGAG-----T--CTGGAAAG--GG-----GTCTGGGGCCCTGGGGAGGCT 1658
 Qy 2207 -----CTCAGGGGACCTCC-----CCAGGCTGGCTCACTGG--AGCG 2244
 Db 1657 GGGGAGTGGGGGCTCA--GGC-----CCGTGCTGCTGGCTTGGTGC-TTGGCAAG--GG 1606
 Qy 2245 AACCGGTGGAGGCTCTCTCAAACTGACAGC-----TC--CCGTGTCTTCCCTGG 2298
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 Qy 2504 GGGGCGGAGCGATG---GG-GA--TACAGACAGC---G-TACAGACCA--TGGTGG 2548
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 Db 1360 TCCGCTTGTATCTGTGCTGCG-----CTCCG--CTGGCGCCGCTCTCTCTCC- 1313
 Qy 2590 GGGGCGGCA--CCATG--GTGTCCAGCGCACCCCTGAAGAGAGCGGAACCTGCTG 2643
 Db 1312 ---GCCGAGAGCC-TGCAATGCTCCAGC-GGCGGCTG-----CTGGCT- 1274
 Qy 2644 CATGCTGACAGATGGGTACAAACTGCG--CTGAGG-TGGTCCAGC-CCAGCCTCT- 2698
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 Db 543 GGTGCGGTCCAGCTGAGCACTCAACCCAAATC-----CACTAG--CTT---GACC 498
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Search completed: April 19, 2005, 10:01:02
 Job time : 28 secs

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T	ITLE		Dan,I., Watanabe,N.M., Kobayashi,T., Yamashita-Suzuki,K.,		
J	URNAL		Fukagawa,Y., Kajikawa,E., Kimura,W.K., Nakashima,T.M.,		
M	EDLINE		Matsumoto,K., Nimomiya-Tsuji,J. and Kusumi,A.		
P	UMED		Molecular cloning of MINK, a novel member of mammalian GCK family		
R	EFERENCE		kinaes, which is up-regulated during postnatal mouse cerebral		
A	UTHORS		development		
			FEBS Lett. 469 (1), 19-23 (2000)		
J	URNAL		20175403		
M	EDLINE		10708748		
R	EFERENCE		2 (bases 1 to 3888)		
A	UTHORS		Dan,I., Watanabe,N.M. and Kusumi,A.		
T	ITLE		Direct Submision		
J	URNAL		Organized (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane		
			Optimizer Project: 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi		
			460-0012, Japan [E-mail:dang@bio.nagoya-u.ac.jp,		
			Tel:81-52-789-2497, Fax:81-52-789-2968]		
			Location/Qualifiers:		
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 Db 2795 -ATGCTGCC--C-CACTGCTTCAG--GCTGTGATCTCTTA-CATCCACAAACATCG 2744
 Qy 1168 --AAAC-A-C-CTGCTGACACAGCGG-----CAGCGGCGCA-TAGA--GG-AG----- 1206
 Db 2743 TGA-ACGAGCTCT--TG--CCAG-GGGCTTTACAGAC--C-CACAGAGCTGTATCTAC 2693
 Qy 1207 -----CA-----GAAGAGAGC--GGC-----GC-----CGGTGTAG- GAGCAAC 1240
 Db 2692 CACTCCATCTCTTCAGAGGTGG--GCTTTGGCTTTCTGTCTTCG- GTGG-GTG----- 2642
 Qy 1241 AGCGGC-GGAGGGGAGAGCGCGGAAGCTGAGG-AG-----A--A--G--G--AG 1281
 Db 2641 AGTGGCTGG--GCTGACCA-CG-----T-CAGGAGGTTTGTATCCCATTCCTGTCCAG 2591
 Qy 1282 CA-GCAGC--GG--CGGCT-----GGAGACATGCAAGCT-----C-TGGG-G-C 1318
 Db 2590 CATGACGACAGTTCC-GCTTCCTTTACAG--GG--TGC--GCTGACACCAATG-GTGGC 2539
 Qy 1319 G-----GGA-GGAGAGC--GGCGG--CAGCGGAGGCTGTAGACAGAAAT-----ACAAG-C 1363
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 Qy 1364 --GGA--ACGAGCTGAG--GAGCAGCGGCACTGAC--AACGTCTCCAGAGCA--GCTGC 1414
 Db 2496 GTGACACACCA--TGTGTCTGA-----C-GCTGTCTGTA--TC-CC-----CATTCCTGC 2453
 Qy 1415 AG-----CAGAGCATGCTTAC--CTCAATCCCTCAGACAGACAGCAAGCAGACAG 1467
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 Db 1784 GGTGCTGCAATAGGCTTCAGTGGAC--CGGTGTG--CCA-----CCAGG-- 1743
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 Qy 2219 TCCCCAGGCTGCTCA--CTGAGCGGAAACCGGTGGAGCCTC--CTCCAAAC-TG 2271
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DB 1167 G-T-GTTT--GATG--TGTG--CCTGGGGGTCT--C-GCTGCT--GC-TGCTGCT 1127
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DB 1021 A--G--CT-TGGCTCTC-C-T--TCCCTCCA-----TGG-CTGTCTCTCC--T 983
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DB 160 -TGATGGC-----AGCCAGCTGCCCGCTTGAATGCGACCT-TGT-----A 118
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DB 117 ----CACTGTCCGTA--GG--TTCCATGCCGACC--AC--CTCCACA-A-GCTCA 75
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GenCore version 5.1.6
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Searched: 1 seqs, 3888 residues

Total number of hits satisfying chosen parameters: 2

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Listing first 45 summaries

Database : ab035698.seq:*

Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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2	2341.6	59.3	3888	1	ab035698 TOIG of: ab03569

ALIGNMENTS

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cde.
ACCESSION AB035698
VERSION AB035698.1 GI:6970477
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases)
REFERENCE Dan, I., Watanabe, N.M., Kobayashi, T., Yamashita, S., Suzuki, K.,
Fukagaya, Y., Kajikawa, E., Kimura, W. K., Nakashima, T.M.,
Matsumoto, K., Minomiyu-Tsuji, J. and Kusumi, A.
TITLE Molecular cloning of MINK, a novel member of mammalian GCK family
kinases, which is up-regulated during postnatal mouse cerebral
development
FEBS Lett. 469 (1), 19-23 (2000)
JOURNAL MEDLINE
PUBMED 10708748
REFERENCE 2 (bases 1 to 3888)
AUTHORS Dan, I., Watanabe, N.M. and Kusumi, A.

TITLE Direct Submission
JOURNAL Submitted (10-DEC-1999) Ippelita Dan, ERATO, Kusumi Membrane
Organizer Project: 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
460-0012, Japan (E-mail: dangebio.nagoya-u.ac.jp,
Tel:81-52-789-2497, Fax:81-52-789-2968)

FEATURES
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Query Match 96.8%; Score 3823.8; DB 1; Length 3888;
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3368	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	1 (sites)	Dan, I., Matanabe, N.M., Kobayashi, T., Yamashita-Suzuki, K., Fukagaya, Y., Kajikawa, E., Kimura, W.K., Nakashima, T.M., Matsumoto, K., Nishimura-Tsuji, J., U. and Kusumi, A.	Molecular cloning of MINK, a novel member of mammalian GCK family kinases, which is up-regulated during postnatal mouse cerebral development	FEBS Lett. 469 (1), 19-23 (2000)
3485	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3486	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3487	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3488	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3489	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3490	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3491	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3492	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3493	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3494	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3495	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3496	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3497	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000	AB035698	AB035698.1	GI:6970477	Homo sapiens (human)	Homo sapiens	2 (bases 1 to 3888)	Dan, I., Matanabe, N.M. and Kusumi, A.	Direct Submission	Submitted (10-DEC-1999) Ippseita Dan, ERATO, Kusumi Membrane Organizer Project, 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi 460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp, Tel:81-52-789-2497, Fax:81-52-789-2968)
3498	LOCUS AB035698	3888 bp mRNA linear PRI 18-APR-2000									

Db 2783 CTGCC-TC-----CAG-G-CTGGTAGA-TC--C-CTA-----GA-----TCCA 2753
 QY 1083 GCAGAGAA-ATAAGAC---AACTCAGAGCT-TTAAAACAGACAGACGCTGCAGC--- 1135
 Db 2752 -C--AAACAT-----CGTGAAC--GA-GCTCTT-----GC--CAG--G--G--GCCCT 2720
 QY 1136 --AGCAGACAG--CAGGAGACCCC-GAG--G--CACACA-T-CMAACA-CCTGCTGCAGC- 1183
 Db 2719 TTA-C--CAGCCCA-CGAGA---CTG-GTAGTCAC-CACTCC---CATCTT-T-----CG 2678
 QY 1184 AGCG---GCAGC---GGC-----GCATAG---AGAGACAGAG-GAG-GAGC-GGCGCG 1226
 Db 2677 AG-GGTGG--GCTTTGGCTTTGG-T-GTTCTCGGTG--G--GTAGTG-GCTGG-----G 2632
 QY 1227 CTTGAGAGAGCAACA-G-C-GGCGGAGAGG--G-G-AGCAGCGGAA-GCTG-CAG--- 1272
 Db 2631 C-TGGA-----C-CAGGTGAGGC--AG-GTTTGTGTACC--C--ATTGCTGTGCAAT 2588
 QY 1273 G-AG-AMAGAG---CAG-----CAGCGCGG--GCTGAGAG-A-CATGAG-GCTCT 1313
 Db 2587 GCAGCA--G-GTTTC-GCTCTCTTTAG-GG-GTGGCTGGA-CCACCATTG-GTGC-C- 2539
 QY 1314 G---CGCGCGG-A-GGAGAGC-GGCGG--CAGGCGGAGCTGAGGAGATACAGC-- 1363
 Db 2538 GCGCC--C--GTATGG-GG-GCTG--GGTCC--CG-----GTGATC-----T-C--CTC 2503
 QY 1364 GGAAGCAG-C-TGAGAGAGC-AGCGGCA--GT-C-A-GAAC-GTCT-----CCAGAGC 1408
 Db 2502 G--A-C-GTCTGTGA-----CCA-C-CATGTGCTAGC--CTGTCTGTATCCC-----C 2461
 QY 1409 A--GCTGAG-----CAGAGCATGCTTA-C-CTCAG--TCC---CTGAGAGCAGCA 1455
 Db 2460 ATCGCTGC-GGCCCCCAGG-G--G-TATCTCT--GCTCCCTCTGTCTG--GC-C-- 2417
 QY 1456 CAGCAGC-AGCAGCTTCAGAAAC---AG-CAG---CA--G---CAGAGCTCTCTG 1497
 Db 2416 C-GC--CTTTCG--CTTC-----CTCTGTGC-GTCTCATCTGCTTTCA-C-CTCC- 2372
 QY 1498 C-CTGGGAGAG--GA--AG-CC---CCTGTACATT--ATGTC--GGGG-CAT-G 1539
 Db 2371 CGCT--GGAC-GACAGTAGTCAATGAGCTT-T--C-TTGGGA-GG-CCGAGGGGCG-TCG 2322
 QY 1540 ---A-TCCCGCT-----G-ACA-MACAG-CTT--GGG--CC-GAAG--GTAG 1576
 Db 2321 TCCAGAGT-CGCTCTTTTCAGAACAA--AGTC-TGGGGCGGCGCTG--GCCGT-- 2271
 QY 1577 AAGAGAAACAAGATGAACAAGACAGACATC-TCC---CTTGG-----CCAGA 1624
 Db 2270 ---GAG--C--GG-TG-----G---TCGT-CGGGCTTGGCTTATTTCC-AG- 2237
 QY 1635 GCAGCCAG-GCAGCAG-GGGGCTGAGGCCCCCATCCCCCAGGCTTCCAG--GGC 1678
 Db 2236 G---G--GAG-AGCAGAGGG---GAGC-----T-----G-TCC--GGTTTG- 2207
 QY 1679 CCCCAG--GACCCCTTTTCCA-GAC---TC--CTCTTA-TGCAG--AGGCC--GGTGA- 1724
 Db 2206 ---AGAGAAC-----TCCACAG-GGTTTCGCTCC-AGTG-AGCCA-GCTGGGG-GGAG 2161
 QY 1725 --GCCCCAG-GAG-GGACC--GCACA-A-----GTCCCTGACGAGACAG--CCCA-CCCG 1769
 Db 2160 GTGGCC--GTAGAGG--CTGG-A-AGAGCGCTGTCC-G-AG--C-GTTCCCAAGC-- 2116
 QY 1770 AAACCTGCTGCTTCCAG--CTTCCATGA--C-----C---C-GACCCTGCT 1812
 Db 2115 --A--GG--G--TC--GCTCTCC--TGAGGTGGGGTTACTGGGACGGA--CTGCC 2073
 QY 1813 AT---C---CCC--GCACCAATGCGCAG--CCCA--GTGCCG---AGAGC--T-GT 1853
 Db 2072 -TGGGCTGGC-CGGG-ACC--CT--C-CGGCCCACTGTG---GTAAAG-GCAGTGG- 2027
 QY 1854 C-ATCCGCAAGATTCAGACCCCA---CCTTGAAGG-ACCT-----GGCCCAAGCC-C 1901
 Db 2026 CGAT-----AGA-T--G-----AGGTCTCTTG-AGGCACTTGGGTGG-----GCTTC 1987

QY 1902 G--AATC-----C---CCCA-GCCTGGTCCGCCAGA-TAAGAGGC-----CCA---C 1942
 Db 1986 GTTA-TGGGGCGAACCCAGG-CTGGG--G---GATT--CG-GG-CTGGGCGCAGTTC 1940
 QY 1943 C--CA-AGGTG---C-----CT--CAGAG--GAC--CTCATTTATC--GCCACT--GC 1979
 Db 1939 CTTCAAGAGTGGGGTGTAAATCTGGC-G-GATGACAGTTC--C--TGGGG-CAGTGGG- 1888
 QY 1980 CC-TTAAAC-CAGTGGG-GCCGG-----AGGTTCC-----C-----GGC----- 2011
 Db 1887 -CGT-----GGCAGTGGGTG-CGGGATGACAGAGT-CGGGATCATGGAGGCTGGAGAG 1836
 QY 2012 -CAGCCCAAG---CAG--TCCG---TGCAGACTTCGA--GCACTCCGCTTGCATAT 2060
 Db 1835 GCAG-CCAGGTTTC-GGGT--GGGCTG--GTCTT-GCAGGG--ACT-G--GG--AT 1794
 QY 2061 C---TA-----T-CTGCAA-A-GGC-----G-GGCAGAGC--GG-G-GCACCCMAAGCT 2100
 Db 1793 CGGGGTACAGTGTCTG-ATATGCTTCAGTGG--GA-CCCGTGTG-----CCA----- 1748
 QY 2101 CCAGGACCCC-C-TGCT-CAG--CCC-CCT-GGCGCG-CCAAC--GCCTTAATTAACC 2150
 Db 1747 CCAGG---CTCTTG-TGC-GGTCCCTCTGGG--GCTTC-ACCAGCCTCT-G----- 1705
 QY 2151 GCACCTCAGAGAGACGACCTGTGGG-AACGCTCGACAGCCTCTTCCAGCCTTC 2209
 Db 1704 C-A-T-AGAGAGAG-----T--CTGGGAA--GG--G-GTCTT--G----- 1676
 QY 2210 ACG-GGACACTCCCGAGGCTGCTCA---CTGAGCGGAA-CCGGGTGGAGCTTC---C 2262
 Db 1675 --GGGAG-CTT-----GG--GG--AGGCTGG-G-GGA-TG-G-GGG-G-CTCAGGC 1638
 QY 2263 TCCAAAC-TGACAGCT-CCCCTG--TGCTTCCCTGGGAATTAAGCAA-GCCCGAC 2316
 Db 1637 -CC--CGT-----GCTGC--CTGGCTGTCTT--TG-----GCCAAG--GA- 1605
 QY 2317 GA-----C-----CA-CC--G---CTC---AGGC---CAGGCCGCCGCCA-G 2347
 Db 1604 GAGTCTGTCTGTGTTATCTTGTCTCTTCTTAC--CTCTC--G--GGCC--CAGG 1553
 QY 2348 ACT--TTGGTGTGTAAGAGAGC-GGACTGTGAGCA-GGCCCTCGG-CC-TCCAA-- 2399
 Db 1552 -CTGTT-TGT--C-----ACGGGA-T-T--C-ATG-CCCC--GACCAT--AATG 1516
 QY 2400 G-A-AGGCCATGACTACTCTGTC-GT--CAAGC-AGAG--G-TGAAAGAGTAGAGA 2450
 Db 1515 GTACAGG---GG-CT--TC--CTGTCCAG-GAAGAGCTGCT-----GC--TG----- 1477
 QY 2451 C-GACGAGAG--GAAG-GCGAAG--GC-G--G--GC--CAGCAGGGGAGC-- 2490
 Db 1476 CTG-C--TGTTCTGAAGCTGC--TGCTGTGTTGCTGCTGCTGCA---GGGA-CTTG 1428
 QY 2491 AGAGATA--C---C-CTGGGGGCGC-GCAGGATG-----GGGATACAGACAG--GTCA 2536
 Db 1427 AG-G-TAGGCAATGCTCTG--CTGCAGC-TGCTCTGG-----AGAC-GTTC-T-- 1386
 QY 2537 GCACCATG--G-TGG-----TCCACAGC-G--T-CGAG--G-AGAT-CAC-----CG-- 2572
 Db 1385 G-AC--TGCCCT-GCTCTTCA-G-CTGCTTC--GCTTGA--TTC-CTGCTGGCGCT 1337
 QY 2573 --G--GAC--CCAGC-CC-CCATAC--G--GGGG-G-GCAC-CATGTGG-TCCAGC 2614
 Db 1336 CCGGCTG-CCGCC-GCTCTTCC-T-CCGCGG--CAGAGC-CTGCAT-GT-CCTCCAGC 1287
 QY 2615 GCAC-CC-CTGAAGAGAGC-GAAG--C-TGCTGATGTGAGAGCAAT--G--GGTA 2663
 Db 1286 --GGCGCT-----GCTG--CTCTT-CT-C--CTG-CAGC--TTCCGCTGCT- 1250
 QY 2664 CACAAAC-CT--GCTGACGTG--G-----TCCA-----GC-CCAGC-CACTCAG--C--C 2703
 Db 1249 C-C---GCTTCCGCGC-G-C-TGTTGCTCTTCAAGCGGCGCG-GCTC-CTC-CTTCTGC 1200

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OY 2704 ACCGAGAAC-A-GCAAGGCCAAGC--CCACC-CTGC-----A--AGATG--GAGTG 2749
DB 1199 TCC-----TCATGTC-----GCC--GCTG--GGTGACGAGG-T-GTTTGA-TG 1158
OY 2750 -GTGATTAC-CAG--TCTGC-TGGGCTG--G-TAAAGC--C-C-CTG--GC----- 2787
DB 1157 TGGG-C-CTC-GGGGCTTCGCT--GCTGCTGCT--GCTGACGCTGCTGCTGTTT 1108
OY 2788 -AAGAG-CTC--GTTACG--ATGTT--TG-TGGA-----TC-----T 2816
DB 1107 TAA-AACCTCTGAGTT--GCTTTAT-TTTCCTGCTGAGCCGAGAACTCCGCGT 1053
OY 2817 AG-G--GA-TCTACCA-GC-CTG-----GA-GGAG--TGGGACAGATCC--CCATCA 2860
DB 1052 AAGATGACACTCT-CCAGGAC-GTTCATATG-AGCTTGG--C-TG-TCTTCC-T-- 1004
OY 2861 CAGC-CTTAGTG--GTGAGAGGCA-----CTGAGCTC--GACCACTG--CAGT 2905
DB 1003 ---CTGC-A-TGGCTGT-----CATCTTCTC-CTGCTG-CC-GCTGTACTCA-T 962
OY 2906 A--C-G-----A-----T--GAGAA--GGGTC--TGTGTC--A 2932
DB 961 ATTCTCTCTCTTTTCTCACCCCGCTTCTCCG-GG-ATCG--TCATGTGCTCTTA 906
OY 2933 AGC-T-GAATCCC--ACCAACAC--CCGAGC-CCACAGT-GAGACCCCTGAGAT-CCGGA 2983
DB 905 A-GCTGG-AT-GGGGAC-----CTGCC--GCTCC--GTGG-G-----CTG-G-TCCCGA 866
OY 2984 AGTACAAGAA-GCGATTCAAC-TCCGAGAT--C-CTC-TGTGACGCCCTTTGG--GG 3032
DB 865 --T-----GAAGG-GA--AACTTC-AG-TAGCTGCTCCGTG-G--G-----TGGCGCG 827
OY 3033 ---GTCACACCTG-CTGGTG--G-GCAC--G-G--A-GAAGGG--C-TGA-----T 3068
DB 826 TCAAGT-AA--GCTC-TGATAG-A-CATGTCTAATGAA--GTCAATGAATCTTCTTA 777
OY 3069 G-----TTGC-TGACC--GAG--TGAGC--AGGG--C-AAGG-TGTATGA----- 3105
DB 776 GACCACTT-CTTGA-CTTG-AGCTGGGCGAGGGTTCCGA-GGATG-A-GGAAGAG 723
OY 3106 -CT-CATTGGGGG-GGACGCT-TC-CAGCAATGATGTCTGAGGGGCTCAACTG 3159
DB 722 GCTCGCA-TGGG-GTGC-A--TGTACA-CAGA-----G--GG-GGGGCTC--CT- 683
OY 3160 CT-CATCACCATCTCAGGAA--GGAACAACTGGGGGTATTACTGTCT-GGCTC 3216
DB 682 CTGC-----CATCTC--G--ATGC-----CT--GTG-AT-----TCTTAG-- 655
OY 3217 CGGA-A-CAAGAT-T-CTGCAC--AATGACC--AGAAGTG-AGAAGACAGAG-- 3263
DB 654 ---AGACCA-AATCACT-C-CTGTAAT--CATAG--GTGGCA-----TCAGGGTT 613
OY 3264 CTGAGCA-C-C-GTGGGGGAC-ATGAGGGG-TGC-GG-GCACTA-CC-GT-GTTGTGA 3313
DB 612 CT-----CATCAG--G-CGAT-GA--CCT-CTGAGC-C-ATCCAGTAG--G-GA 573
OY 3314 ---AATGAGCGGATTAA--GTTCTGTGATGCGCTCA--GAG--C--TCCGTG 3361
DB 572 GTCCCAAT-----GA--AAGTTTC--GTC-T-GCCC--ACG-GTGGGTG--- 534
OY 3362 AAG-TGTATG-CTGGGC-CCCCAA--CC-CTA-----C-CA-CAATTATGAGCT 3406
DB 533 A-GCTG-A-GCACT--CACCCAAAATCAGTGAAGCTGACCTGAG--ATTG-T---CT 486
OY 3407 -TCA-AGTC-C-TT-TGCCGACC--TCCCAACCGCCTTGC-TGG-TGACCT- 3452
DB 485 GTGAGCAG-CACATCTGCC--CTTGAT-----G--TCT-CGATGATC-ACCTT 442
OY 3453 ---GACAGTAGAGAG--GGG-CAG--CGGCTC-AAAG-TGATC-----TAT-GG 3491
DB 441 GTGGG-CA-T--GAGATGGGCCAAGC--C-CTGA-GGATC-TCCCTGCAGATATAG 392
OY 3492 C--T-CCAGTGC-----T--GGC-TT-CCAT--GCTGT-----GGAT--GTGCA 3524

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DB 391 CGATAC-AGT-CCTCCTCAGGCGCTTGC-TTGTG-TGTTCTTTACAGG-TCACTC-A 338
OY 3525 CTGGGGAA-CAGCTATGACATCTACA-----TCCGTGCA-CATCAGAGCAGATCA 3578
DB 337 CT--GAACAGC--AC--C-ACAGACTC-----CATCA-CC-AGCCAG-- 302
OY 3579 GCGCCAT-GCCATATC-TTCTCCCAACACGAGCGATGAGATGCTGTGTC-TA 3635
DB 301 GC-----TGG--TCATGTT--TC-----CG--GG--GG--GCT-CT-T-CTT- 271
OY 3636 CCA-GGACGAGGTG-TCTACTCAACAGTAG--GGCGATCATTAAG-GATGTGTG 3690
DB 270 -GATG-A--AG--GCTC--CGT--A-GTA-GGTGGCG-AT-GTT-GCG--GTGGTG 232
OY 3691 ---CT-----GCA-G-TGGGGGAGA--TGCT-----ACT-TCTGTGCGCTACAT 3728
DB 231 AAGTACTTTTTCAGATGTT-----GATCT-CCTGTTGA-TCTCT-T--CTT-C-- 187
OY 3729 CT-G-CTCC--A-A-CCA-GA--T-AATG--GCTGGG--G--TGAGAA- 3761
DB 186 CTGCTCTCCGAGATCAATCACTGA-TGGAGCCAGCT--GCCCGCTTG--AC 133
OY 3762 A-GCATTGAGATCGGCTGTGAGACGGCCACT--CG-ACGGGCTTT-CA-TGC 3814
DB 132 ATGCC-----GA-CC-CT-TGT--A-----CACCTGTCCGTA--GG--TTCCATTGC 95
OY 3815 --A-CAAAGACT--CAGAGGCTC-ANG-TTCTGTGTGAGCGGATGACAGATGTT 3866
DB 94 CGACC--AC--CTCACA-A-GCTCAAGAT-CC-----C--A-G-C-AGG-GT- 59
OY 3867 TTTTGCTCAGTCC-GCTGTGGG-GGACAGACCAAGTTACTTC-ATGACTC-TGACC 3922
DB 58 ---CC-C-G--CAG-----GGCGG-A-CAG--G-----TGATG--TGT--CC 30
OY 3923 GTAA-CTGCAT-CATGAATGG--TGAAAG--GC 3951
DB 29 ---AGGCTGC-GAGC--G-----GGGCTG--GGTGC 5

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Search completed: April 19, 2005, 10:03:32
 Job time : 29 secs

US-10-029-115-2 (1-1312) x ab035698 (1-3888)

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 QY 21 ProAlaGly11IlePheGluLeuValGluValAlaGlyAsnGlyThrTyrgGlyGlnVal1Ty 40
 Db 61 CTGTGCGGATCTTTAGCTTGTGGAGGTGGTGGCAATGGAACTTACCGAGACAGGTATAC 120
 QY 41 TyrgValArgHisValIleTyrgGlyGlnLeuAlaAla11IleValIleMetAspVal1ThrGlu 60
 Db 121 AAGGGGTGGCATGTCAAGACGGGGGACGTGGCTGCATCAAGGTCTCATGTGATGCACGGAG 180
 QY 61 AapGluGluGluGlu11IleTyrgGlnGlu11IleAsnMetLeuIleValTyrgSerHis1Arg 80
 Db 181 GACGAGAGAGAGAGATCAAAACGAGATCAACATCTGAAAAAGTACTTCCACCAACCCG 240
 QY 81 Asn11LeuAlaThrTyrgTyrgGlyAlaPhe11IleTyrgSerProProGlyAsnAspAspGln 100
 Db 241 AACATGCCACCTACTACGAGAGCTTCAACAGAAAGACCCCGGAGAAACATGACAG 300
 QY 101 LeuTrpLeuValMetGluPheCysGlyAlaGlySerVal1ThrAspLeuValIleAsnThr 120
 Db 301 CTCTGCTGATGTGAGATTCTGTGGTGTGCTGTTCACTGATGACTGCTGGTAAAGAACACA 360
 QY 121 TyrgValAsnAlaLeuTyrgValAspCys11IleAlaTyrg11IleValArgGlu11IleLeuArgGly 140
 Db 361 AAAGGCAAGCCCTGAAAGAGAGACTGTATCTGCTAATCTGACGAGAGATCCCTCAGCGGGT 420
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 QY 161 LeuThrGluAsnAlaGluValIleTyrgLeuValAspPheGlyValSer11IleGlnLeuAspArg 180
 Db 481 CTGACAGAGATGCTGAGGTCAAGCTAATGTGATTTGGGGTGAAGTCTCAGCTGACGACCG 540
 QY 181 ThrValGlyValArgAsnThrPhe11IleGlyThrProTyrgTrpMetAlaProGluVal11Ile 200
 Db 541 ACCGTGGGAGAGACGGAACACTTTCATTTGAGACTCCCTACTGATGTGCTCAGAGGTGATC 600
 QY 201 AlaCysAspGluAsnProAspAlaThrTyrgAspTyrgSerAsp11IleTrpSerLeuGly 220
 Db 601 GCTGTGATGAGAACCTGATGCCACTATGATTAACAGAGTATTTGGTCTTACGAA 660
 QY 221 11IleThrAla11IleGluMetAlaGluGlyAlaProProLeuGlyAspMetHis1ProMetArg 240
 Db 661 ATCAGACGATCGAGATGAG 720
 QY 241 AlaLeuPheLeu11IleProArgAsnProProProArgLeuIleValTyrgSerHis1Arg 260
 Db 721 GGCCTCTTCTCTCAATCTCGGAACCTCCGCGCAGAGCTCAAGTCAAGAGAGTGTCTAAG 780
 QY 261 TyrgPhe11IleAspPhe11IleAspThrCysLeu11IleTyrgThrLeuSerArgProProThr 280
 Db 781 AAGTTATTTGACTTCTTACACATGTCTCATCAAGACTTACTGAGCGGCCCAACCCAG 840
 QY 281 GlnGlnLeuLeuIleTyrgAspPhe11IleArgAspGlnProThrGluValArg11Ile 300
 Db 841 GAGCAGACTAGTAAGTTTCCCTTCATCCGGGACCAAGCCAGAGGAGGAGGAGGAGGAGGAG 900
 QY 301 GlnLeuIleTyrgAspHis11IleAspArgSerArgIleValArgGlyGlu11IleValArgGlu 320
 Db 901 CAGCTTAAAGACCACTTGAACCATCCCGAAGAACCGGGGTGAGAAAGGAGGAGAGACAGAA 960
 QY 321 TyrgGluTyrgSerGlySerGluGluGluIleAspAspSerHis1GlyGluGluGluIleProSer 340
 Db 961 TATGAGTACAGCGGACGAGGAGGAGAGATGACAGCATTGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 341 Ser11IleMetAsnValProGlyIleSerThrLeuArgArgGluPheLeuArgLeuGlnGln 360
 Db 1020

Db 1021 TCCATCATGAACGTGCTGGAGAGTGCATCTTACGCCCGGAGATTCTCCGAGCTCCAGCAG 1080
 QY 361 GluAsnTyrgSerAsnSerGln11IleValTyrgGlnGlnGlnGlnGlnGlnGlnGlnGln 380
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 / VERSION AB035698.1 GI:6970477
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 / ORGANISM Homo sapiens
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 / 1 (sites)
 / REFERENCE Dan, I., Watanabe, N. M., Kobayashi, T., Yamashita-Suzuki, K.,
 / Fukagaya, Y., Kajikawa, E., Kimura, W. K., Nakashima, T. M.,
 / Matsumoto, K., Niimiya-Tsuji, J., and Kusumi, A.
 / Molecular cloning of MINK, a novel member of mammalian GCK family
 / kinases, which is up-regulated during postnatal mouse cerebral
 / development


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JOURNAL      FEBS Lett. 469 (1), 19-23 (2000)
MEDLINE      20175403
PUBMED       10708748
REFERENCE    2 (bases 1 to 3888)
AUTHORS      Dan, I., Watanabe, N.-M. and Kusumi, A.
TITLE        Direct Submission
JOURNAL      Submitted (10-DEC-1999) Iipelta Dan, ERATO, Kusumi Membrane
              Organizer Project; 5-11-33 Chiyoda, Naka-ku, Nagoya, Aichi
              460-0012, Japan (E-mail: dang@bio.nagoya-u.ac.jp,
              Tel: 81-52-789-2497, Fax: 81-52-789-2368)
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25 e-GluLeuValGluValValGlyAsn-Gly-----ThrTyrGly-----G1 38
3861 CAGAGTGC-AT-GAAGTA-----AACTGGCTGCTGCCCCAGAGC--GGACTGAGCA 3813
38 n-----Val-TyrLysGlyArg-HisVallysrthrglyGlnLeu-Ala-----A1 52
3812 AAAAAACACCTTCTCATTC-----GGCTCAC-----ACAGAAC-TTGAGCTCTGAGC 3766
52 a-IleLysVal-Met--Asp---ValThrGluAspGluGluGluIle---LysGln 69
3765 TCGTTT--GTGATAGAGACCCCGTC-----GAGTGGCCGCT--- 3730
69 LuileAsnMetLeuLysTyrSerHisIleArgAsn-IleAlaThrTyrTyrGlyAl 88
3729 -----CTC-----CACAGAGC-GGATC--TCAT--GGCT- 3705
88 aPheIleLysLysSerProProGlyAsnAspAspGln--Leu--TyrLeuValMetG1 106
3704 -TTT-----TCACCC-----CAGCCCATTAATCTGGTTG-----GA 3676
106 uphe--Cys-GlyAlaGlySerValThrAspLeuValLysAsnThrLysGly----- 122
3675 GCA-GATGAGGCC-----ACAGAA--GTA-----GGCATCTCCC 3643
123 -Asn-----Ala-----LeuLysGluAsp--CysIleAla--TyrIleCys--ArgG1 136
3642 CCACGTGACACACACATCCTT-----AATGATGC--GCCGTAGC--TGTTGAGCT- 3596
136 uIleLeuArgGlyLeuAlaHis-----Leu---His-Ala-HisLysValIleHis- 151
3595 -----AGA-----CACCTGCTCTGCTGTAGCAGAGCAT-----CTCCAG 3558
152 -ArgAspIleLysGlyGlnAsnValLeuThrGlnGlnAlaGluValLysLeuValAs 171
3557 CCGTGC-----GTG-----TTGGG-GAG-----GAA-----GA 3536
171 pPhe-----GlyVal-Ser-AlaGlnLeuAspArgThrValGlyArgAsnThrP 188
3535 TGA-TGGCATGGGGGTATCTGGCT--CTGAT-----GTGC-----ACA- 3498
188 heIleGlyThrProTyrTrpMetAlaProGluValIleAlaCysAspGluAsnProAspA 208
3497 -----GGG-----ATGT--A-GATGATATAGC--TGTT-----CCC--- 3472
208 laThrTyrAspTyrArgSer-AspIle-----Trp-----SerLeuGlyIleThr--- 222
3471 -----CGAGT--CGACATCCACAGCATGAAAGCCAGC-----ACTGGA 3436
223 AlaIleGluMetAla--GluGly--AlaProProLeu-CysAspMetHis-----ProM 239
3435 GCCATAG-ATACCTTGAGCC-GGCGCCCTCTCTACTGT-----CAGTCCAGCCAG 3385
239 eCArg-----Ala-----Leu-----Phe-----L 244
3384 C-AGAGGCGGTGGGAGAGTGGGCAAGACTTGAAGCCATGATTTGTGTAGGGTT 3326
244 euIle--ProArgAsnPro-ProProArgLeuLysSerLysLysTrpSerLysPheI 263
3325 TGGG-GGCCAGCAGCATAC-ACCTCCAGG-----AGC-----TCTT----- 3292
263 leAspPheIleAsp--ThrCys--LeuIleLysThrTyrLeuSer----- 276
3291 --GAGG--GC-GATGACAG-GAATTAATCCGCTCGTATT--TCAACAACAGGTAGTGC 3240
277 -Arg-----Pro-----ProThrGlu--Gln--LeuLeuLysPhe-Pro-Phe--- 288
3239 CCGCAGCCTCCATGTCGCCACAGGT-GGTCCAGCCCTGCTTC--TTCTCCACTTCTGGG 3183
289 --IleArgAspGln-----ProThrGlu--Arg-GlnValArgIleGlnLeuLysA 304
3182 TCATTG--TG-CAGATCTTGTTCG--GAGCCAGGACAGGTA--ATA----- 3142

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OY 304 apHieIleapRtSerArgLyLeuArgGlyGluLeuGluGluThrGluTyrGluTyrS 324
DB 3141 ---CACC-----CGCACTT---TG-----TTCC---TTTT 3121
OY 324 ergLySerGluGluLeuAapSerHieGlyGluGlu---Gly-Glu-ProSerSerile 342
DB 3120 CCTT-GA-----GAT-----GGTATGACAGAGTTGAGCCCTCCACACA-- 3083
OY 343 MetAenValProGlyGluSerThrLeu---ArgArgGluPheLeuArgLeuGluGlnI 361
DB 3082 ---CAT---CCA-----TCTG---CTGGAAGCGTCC-----CGCC---CAAT---GA 3050
OY 361 uAenLySerAen---SerGluAalaLeuLySgInGlnGlnIleu-----GlnGlnGng 379
DB 3049 G-----TCAT-ACACCTT-GCCCTGCC-CA-----CTTCGGCTCCAGCAACATC 3009
OY 379 InGluArgAap-ProGluAaHieLySgInGlnGlnIleuArg---Arg-----G1 395
DB 3008 AGCC-CGTTC-TCCGT-GCC-----CACACAGAGGTTGACCCCCCA 2971
OY 395 nArg-----ArgIle---GluGluGlnLySgInGluArg-----Arg-- 406
DB 2970 AAGGCTGCACAGAGGATCTCGAAGTT-----GAAT---CGCTTCTTACTTCGCGAT 2920
OY 407 ---Arg-ValGluGlnGlnIle---Arg-----Arg----- 414
DB 2919 CTCAGAGGCTCT-----CAGCTGGCCCCGGGCTTGGAGATTCAGCTTGACACA 2868
OY 415 Glu-----ArgGluGlnArgLyLeuGln-----GluLySgIn-----G1 426
DB 2867 GAACCTTCTCCACGT-----CGTA---CTGACGCTGTCGAGCC-GATGGCCCTCTCCA 2817
OY 426 n-Gln-ArgArgLeuGluAap---Met-----GlnAaIa-LeuArgArgGluGlu 441
DB 2816 CCCACTAGGG---CTGT---GATGGGATGCTGTCTCCACATG-CCTCC--AGGC--TG-GT- 2768
OY 442 Arg-----Arg-----GlnAaIaArgGluGlnGluTyrLyAapLyS-----Gln--- 455
DB 2767 AGATCCCTAGATCCACAAACAT---CGTGA-----CGAGC-TCTTGCCAGGGG 2723
OY 456 ---LeuGluGlnGlnIle---Arg-----GlnSerGlu-----Arg----- 464
DB 2722 CCTTAC-----CAGCCACGAGACTGTAACACACTCCA-TCTTCGAGGGGGG 2669
OY 465 -----LeuGln-Arg-----Gln-----LeuGlnGlnIleHie---Al 474
DB 2668 TTGGCTTTGGCTGT---CTCGGTGGGTAGTGGCTGGCTG-----GACACAGTCAGGC 2616
OY 474 a-----Tyr-----LeuLySerLeuGlnGlnGlnGlnGlnGlnIle----- 487
DB 2615 AGGTTGTGTACCCATG-----CTGT-----CAGCATG-CAGCAGGTTCCGCTC 2572
OY 488 ---LeuGlnLySgInGlnGlnGlnIle-----LeuLeuPro-----GlyAapArgLyA 503
DB 2571 CTCTT-----CAGGGGTGGCTGCA-CACACATGTGTC-CGCCC-CC 2533
OY 503 oLeuTyrHieLyGly-----ArgGlyMetAen---ProAlaAap---Lys---Pro 517
DB 2532 G-----TATGGGGCTGGGCTCCCGGT-----GATCTCTTC-GAGCTGTCGAGACA 2489
OY 518 AlaTyr-Ala-ArgGluValGluGlu-----ArgThrArgMetAenLySgInGlnI- 533
DB 2488 CCATGCTGTACGCT---GTCTG-TA-TCCCATGCTG-CGACC-CC-----CAGGG 2442
OY 534 -----Asn---SerPro-----LeuAlaLySerLySgInGlnGlnIleProGluPro 550
DB 2441 GATCTGTGCTCCCTCTGCTGCTGCGC-----CCT---TCG-----CCTT---CTTCC 2400
OY 550 o-Ile-ProGln-AlaSerProGlyProProGlyProLeu-----SerGlnThrPro 566
DB 2399 TCGTGTCTCTACTGCTT---CCA-----CTGCTC---G---CTGACAGCAGAGT---AGTCCA 2351
OY 567 ---Pro-Met-Gln-----Arg-Pro-Val---Glu-Pro-----GlnGluGlyProHie 579

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DB 2350 TGGCTTCTTGGAGCCGAGGGGCTGCTCCAGAGTCCGCTTTCAGCA-----CA 2297
OY 579 b-LySer-----LeuGlnAapGlnPro-----Thr-ArgAenLeuAla 592
DB 2296 CAAGCTCTGGGGCCGCGCTTG-----CCGTAGCGGTGTGCTGGGG-TTGGCTT 2246
OY 592 Ia-PheProAlaSer-----His---Aap---Pro-----Aap---Pro-AlaI1 603
DB 2245 T-ATTCACAG-CG-AGACACAGGAGCTGTCTGTTTGAGAGACTCCACAGCGGT 2189
OY 603 eProAlaProThr-AlaThrProSer-----AlaArg-----Gly-AlaIy 616
DB 2188 TCCGCT-CCAGT-GAGCCAG-CTTG-GGAGAGTCCCTGTAGAGAGCTGGAAGACGCTG 2133
OY 616 aIleArg-----GlnAenSerAapPro-----ThrSer-Glu----- 626
DB 2132 TC---CGAGCGTTCACAG-----CCAGGCTGCTCTCTGAGGTGCGGGTTACTG 2085
OY 627 ---Gly---ProGly-----ProSer-ProAenPro-ProAlaTyr-Val-ArgPro-- 640
DB 2084 GCACGAGCTGCTGGGCTGGCTGGG-ACCTT---CCGGCCCCAC-TGTGTTAAGGACAGT 2029
OY 641 ---Aap-AenGluAlaPro-----ProLys-Val---Pro----- 649
DB 2028 GCGCATATAGAGT-CCTGTAGGACACTTG-GGTGGGCTCTGTTATCTGGCGGAGC 1971
OY 650 Gln-----ArgThr-Ser-----Ser-Ile---Ala- 656
DB 1970 CAGCTGGGAGATTCGCGCTGGGCTGGGCTCCAGGTCTTCAGAGTGGGCTGTAATTGCGCG 1911
OY 657 ---ThrAla-LeuAen---Thr-----SerGly-----AlaGly---GlySe 667
DB 1910 ATGACAGCTCTCTCGG-GCATGGGCTGCAAGTGGCTGCGGAGTGCAGGCTCGCGCTC 1852
OY 667 r---ArgPro-----Ala---GlnAlaVal-Arg---AlaArg-Pro-AerSerAen 680
DB 1851 ATGGAGAGCT-GGAGAGCAGCCAG---CTTTCGGGTGGGCTG-GTCTGACAG---GAC 1800
OY 681 SerAlaTyr-----GlnIle---Tyr-LeuGlnArgArgAlaGluArgLyT 695
DB 1799 ---TGGATCGGGATGACAGGCTGTCATATGCTTCAGTG-----GGA- 1760
OY 695 hrProLyProProGly---ProPro-----AlaGln-ProProGly---ProPro 709
DB 1759 -----CCCGGTGTCACACGAGCTGTGCGGT-CCTTCCTGGGGCTTCACCG 1712
OY 710 AsnAlaSerSerAenProAapLeu---ArgArgSer---Aap-----ProGly----- 723
DB 1711 G-----CCT---CTGCATAGAGAGCTGCGGAGAGGGCTCTGGGGGGCC 1669
OY 724 TrpGluArgSer---Aap-----Ser-----ValLeuPro-Ala---Ser---H 735
DB 1668 TGGGG-AGGCC-TGGGGGATGGGGGGCTCAGGCCCGGCTGCTGCGGTGTCTTGCC 1611
OY 735 isGly-----His-----LeuPro-----GlnAla 741
DB 1610 AAGGAGAGTCTGCTGCTGTTCATCTTGTCTCTTACTCTTCGAGCCAGGCT 1551
OY 742 GlySerLeu-GluArgAen-----Arg-----Val---GlyAlaSer---Ser--- 753
DB 1550 GGT---TTGTCAAGCGGATTCATGCCCCGACCATATAGTACAGGGGCTTCTGTCCCA 1494
OY 754 ---Lys-----LeuAapSer-Ser-----ProVal-LeuSerProGly 764
DB 1493 GGCAGAGCTCTGCTGCTGCTGTT-TCTGAAGCTGCTGCTGCTGCTGCTGCT 1442
OY 765 AenLyAlaIa-LysProAap---Aap---His-----A 773
DB 1441 -----CTGACAGG---GACTTGAAGTAGAGATGCTCTGCTGACAGTGCCTTGAGAC 1391
OY 773 rGser-----Arg---ProGlyArgProAlaAapPhe-----Val---LeuLeuLySg 787

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Db      1390 GTTTCAGACGCGGCTGCTCTCT-----CGACGTGC-TTCGCGCTTGATTCTGCTGCG--- 1341
QY      787 IuArthr--LeuAspGluAlaPro-Arg-----ProPro--LysLysAla---MetAspT 803
Db      1340 ---CGCTCCGCTG-----CGCGGCTCTCTCTCCGCGCGACAGCGTGCATG---- 1296
QY      803 yfSerSerSer-----SerGluGluValGluSer-----SerGluAspAspG 817
Db      1295 ---TCTCCAGCGCGCGCTGCTGCTCTCT-----TCTCTGAGAGCTT----- 1258
QY      817 uGluGluGluGluGluGluGluPro--AlaGluGlu--SerArgAsp-----Thr-Pro--- 832
Db      1257 -----CGCGTCTCTCC-CG-CTCCCGCGCG-CTGTTGCTCTCCACCG 1220
QY      833 GluGluArgSerSerAspGluAspThrAspSerValSerThrMetValValHisAspValGlu 852
Db      1219 GGGCGC-CGCTCTC-----TCTCT-TCTGCG-TCTCTTAAGCG----- 1189
QY      853 GluIleThrGluThrGlnPro---ProTyrGlu-----GluGluThr-Met-Val---- 867
Db      1188 -----CGCGTCCGCGCT-GGTGCAGACAGGTGT-TT-GATGATGCGCTC 1150
QY      868 ---Val-----Gln-----ArgThr-ProGluGlu 875
Db      1149 GGGGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGTTTAAAG--CTCT-GAG-- 1095
QY      875 uArgAsnLeuLeuHis-----AlaAspSerAsnGluTyrThrAsnLeuProAspVal 892
Db      1094 -----TTGCTCTT-ATTTCCTCTCTGCG-AGCG--GAG--A--NACTC-CGCGC-GTA 1052
QY      893 --ValGln---ProSerHis--SerProThrGluAsnSerLysGluGlnSerPro-Pro 909
Db      1051 GAGTGA-CTCTCCAGG-CACGTTCA-----GATGG-AGCTT-GGC--TCTCTTCT 1004
QY      910 -SerLysAspGly--SerGlyAspTyrGlnSer-----ArgGly--Leu-----Val 923
Db      1003 CTCCA--T--GGCTGTCAT--C--TTCC-TCTCTGCTGCGCTG--TACTCAATTTCTGT 955
QY      923 LysAlaProGlyLysSerSerPhe--Thr--Met-PheValAspLeuGlyIleTyr-G 941
Db      954 C-----TCTCTTTCTCACCCCGCTCTTTC-----GGGATCGG-TT 919
QY      941 In-----ProGlyGlySer-Gly-----AspSerIleProIleThrAlaLeu-ValGly 956
Db      918 AATGTGTCTCT--A--AGCTGATGCGGAC--CTGCGG-----CTCGTGGGGCT 875
QY      957 -----Gly-GluGlyThrArgLeuAspGln-----LeuGlnTyrAspVal--ArgLys 971
Db      874 GGTCCCGGATGAAGG--AAACTT--CAGTAGCTGCTCCGTG--GTGGCGCGC-- 827
QY      972 GlySer-Val-Val-----Asn-----ValAsnProThr-Asn--Thr---ArgAlaH 985
Db      826 ---TCAAGTAAGTCTTGATGACAGCATGTCTCAATGA-AGTCAATGAACCTTTAGAC--C 773
QY      985 1s-Ser-----GluThrProGluIleArgLysTyrLysArg-Phe-----Asnse 1000
Db      772 ACTTCTTGACTTGA--CCTG--GG-CGG-----AGGGTCCGAGGATGA 731
QY      1000 r-----GluIleLeuCybAlaAlaLeuTyrGlyValAsnLeuValGlyThrGluAsnG 1019
Db      730 -GGAGAGAGG-CTC-----GCA--TGCG--GTGCG-----GTCAAC-ACAGAGG-G 692
QY      1019 1y-----Leu-Met-LeuLeuAsp-----ArgSerGlyGluGlyLysValTyr 1032
Db      691 GGGCTCCCTCTGCTCATCTGATGAGCTGT-GATTCTCTAGG-AC-CAAA-----TA 645
QY      1032 rGlyLeu-----1leGlyArg-----ArgArgPhe-Gln--Gln--MetAspValLe 1046
Db      644 TCA-CTCCGTAATCAT-AGGTGCGATCAGG--TTCTCATCAAGGCGATGAC-CT-CT 591
QY      1046 uGluGlyLeuAsnLeuLeuIleThrIle-SerGlyLysArg-----Asn-Lys--- 1061
Db      590 GGAGCC-----ATCCAGT-----AGGAGTCCCAATGAAGTGT 556

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QY      1062 ----Leu-----Arg-----ValTyrTyrLeuSerTyrPheArgAsn-LysIleLeuHis-A 1077
Db      555 CGGTCTGCCACGAGGCGGTCTCC--AG-CTGACGA--CTCAC-CC-CAAAATC---CACAT 506
QY      1077 snAsp--ProGluValGluLysGluGlnGlyTyrThrThrValGlyAspMetGluGlyCy 1096
Db      505 GCTT-GACCT-----CAGC-----ATT-----CTC-----TG 485
QY      1096 sGly-----HisTyrArgValValLysTyrGluArgIleLysPhe-----Leu-Val--- 1111
Db      484 TCA-GCAGCACA-----TTCTGCCCTTGATGCTTC 455
QY      1112 -----1leAlaLeuLysSerSerValGluValTyrAlaThrAlaProLysProTyrHisL 1130
Db      454 GATGATCACC-CTT-----GTGG--GCATGGAG----- 430
QY      1130 yspPheMetAlaPheLysSerPheAla-AspLeuProHisArgProLeu-Leu-----Val 1147
Db      429 -----ATGG-----GCCAGAC--CCCTG-AGGAT-CTCCCTCCAGATATA 394
QY      1148 ---AspLeuThrValGluGluGluGln-Arg-----LeuLysValIleTyr--Glyse 1163
Db      393 GCGCAT--ACAGTCT-CC-TT-CAGGCGGTGCTTTGT--GTCTTTACAGATC- 343
QY      1163 rSerAlaGlyPheHisAlaValAspValAspSerGlyAsn-SerTyrAspIleTyrIleP 1183
Db      342 -AGT-----CACTG-----AMCAGCA-----C 326
QY      1183 roValHisIleGln--SerGlnIleThr--ProHisAla-IleIle-PheLeuProAsn 1200
Db      325 CA-----CAGAACTCC--ATCACCGACGACG-GGTGTCATCGTTT--CCC-- 285
QY      1201 ThrAspGlyMetGluMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 1219
Db      284 -----GGGG--GG-CT-CTTCT-----GATGAAGGCTCGTA--GTA----- 253
QY      1220 TyrGly--Arg-Ile---1leLysAspVal---ValLeu--GlnTyrGlyGluMet 1234
Db      252 ---GGTGGGAGTGTGCGGTG-----GTGAGAGTACTTTTCAGC-----ATGTTG 210
QY      1235 ---ProThrSerValAlaTyrIleCysSer-----AsnGlnIle-Me 1247
Db      209 ACTCTCT-----GTTT--G-ATC--TCTTCTCTCTGCTCTCGTGCATC--ATCCAT 166
QY      1247 rGly-----TyrGly--GluLysAla--Ile--GluIle-ArgSer--ValGluThrG 1262
Db      165 GAC-CTTGATGCA-GCCAGCT-GCCCGGTCTTGACATGCCAGC-CTTGA----- 118
QY      1262 yHisLeuAspGlyVal--PheMetHisLys--ArgAlaGlnArgLeu---LysPheLeuCy 1280
Db      117 -CACTGT--CC-GTAAAGTTC--CATTG-CCGAC-CAC---CTCCACAG--CTCA- 75
QY      1280 sGluArgAsnAspLysValPhePheAlaSer---Val-ArgSerGlyGlySerSerGlnV 1299
Db      74 -----AAGATCCC-----AGCAGGGTCCGCGAG-GGCGGA-----CAGG 42
QY      1299 aLysrPheMetThrLeuAsnArgAsnCybIleMetAsn-----Tyr 1312
Db      41 TCG-----ATGTG--TCCAGGC--TGCGG-GC-GG-GGCGTGG 10

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Search completed: April 19, 2005, 10:17:06
 Job time : 46 secs